

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:44:20 ; Search time 18 Seconds
(without alignments)

108.988 Million cell updates/sec

Title: US-10-067-482-2_COPY_271_308

Perfect score: 200

Sequence: 1 GFLGLMGSGIVSNLLKMGHTVWNRVTAEKCDLFIQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/2/iaa/5A COMB.pep: *
2: /cgn2_6/prodata/2/iaa/5B COMB.pep: *
3: /cgn2_6/prodata/2/iaa/6A COMB.pep: *
4: /cgn2_6/prodata/2/iaa/6B COMB.pep: *
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep: *
6: /cgn2_6/prodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	83.0	547	4	US-10-164-595-72
2	124	62.0	345	4	US-09-364-230-8
3	117	58.5	360	4	US-09-364-230-4
4	106	53.0	299	4	US-09-328-352-7407
5	102	51.0	326	4	US-09-328-352-8139
6	100	50.0	299	4	US-09-107-532A-5109
7	98	49.0	295	4	US-09-252-991A-24727
8	85	42.5	204	4	US-09-198-452A-376
9	84	42.0	304	4	US-09-489-039A-9424
10	81	40.5	247	4	US-09-364-230-2
11	80.5	40.2	307	4	US-09-489-039A-9294
12	77	38.5	330	4	US-09-252-991A-17923
13	75	37.5	221	4	US-09-252-991A-22003
14	75	37.5	474	4	US-09-134-001C-3241
15	74	37.0	490	4	US-09-489-039A-8350
16	73	36.5	474	3	US-09-058-692-2
17	73	36.5	474	4	US-09-584-628-2
18	72	36.0	486	4	US-09-543-681A-5380
19	69	34.5	324	4	US-09-252-991A-26001
20	68	34.0	74	4	US-09-621-976-6407
21	68	34.0	350	4	US-09-364-230-12
22	67	33.5	292	4	US-09-711-164-438
23	66	33.0	342	4	US-09-364-230-6
24	65	32.5	154	4	US-09-252-991A-29293
25	65	32.5	543	4	US-09-252-991A-27650
26	64	32.0	303	4	US-09-489-039A-12361
27	64	32.0	321	4	US-09-489-039A-10010

Sequence 923, Ap
Sequence 2874, Ap
Sequence 3137, Ap
Sequence 4004, Ap
Sequence 32, Appl
Sequence 7231, Ap
Sequence 6406, Ap
Sequence 7169, Ap
Sequence 7441, Ap
Sequence 13778, A
Sequence 4879, Ap
Sequence 4, Appl
Sequence 7, Appl
Sequence 13223, A
Sequence 4723, Ap
Sequence 32168, A
Sequence 24, Appl
Sequence 5053, Ap
Sequence 30567, A
Sequence 105, Ap
Sequence 11, Appl
Sequence 3777, Ap
Sequence 4316, Ap
Sequence 4, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 7146, Ap
Sequence 4095, Ap
Sequence 5021, Ap
Sequence 3551, Ap
Sequence 32, Appl
Sequence 10351, A
Sequence 10528, A
Sequence 17150, A
Sequence 62, Appl
Sequence 6279, Ap
Sequence 1748, Ap
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 25, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 3055, Ap
Sequence 440, Ap
Sequence 7202, Ap
Sequence 4, Appl
Sequence 4, Appl
Sequence 13474, A
Sequence 5237, Ap
Sequence 33108, A
Sequence 5065, Ap
Sequence 11014, A
Sequence 6726, Ap
Sequence 1, Appl
Sequence 29547, A
Sequence 10777, A
Sequence 2, Appl
Sequence 2, Appl
Sequence 335, Ap
Sequence 3409, Ap
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 7503, Ap
Sequence 13595, A

ALIGNMENTS

```

RESULT 1
US-10-164-595-72
; Sequence 72, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent version 3.1
; SEQ ID NO 72
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-595-72

Query Match      83.0%; Score 166; DB 4; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEK 32
Db      271 GFLGLGMSGIVSNLLKMGHTVTVMNRTAEK 302

RESULT 2
US-09-364-230-8
; Sequence 8, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Glycine max
US-09-364-230-8

Query Match      62.0%; Score 124; DB 4; Length 345;
Best Local Similarity 64.9%; Pred. No. 1.2e-09;
Matches 24; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFI 37
Db      55  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFI 91

RESULT 3
US-09-364-230-4
; Sequence 4, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni

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; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays
US-09-364-230-4

Query Match      58.5%; Score 117; DB 4; Length 360;
Best Local Similarity 63.6%; Pred. No. 1.3e-08;
Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEK 33
Db      69  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEK 101

RESULT 4
US-09-328-352-7407
; Sequence 7407, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7407
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7407

Query Match      53.0%; Score 106; DB 4; Length 299;
Best Local Similarity 52.9%; Pred. No. 3.7e-07;
Matches 18; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCD 34
Db      14  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCD 47

RESULT 5
US-09-328-352-8139
; Sequence 8139, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8139
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8139

Query Match      51.0%; Score 102; DB 4; Length 326;
Best Local Similarity 52.8%; Pred. No. 1.5e-06;
Matches 19; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY      2  FLGLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFI 37

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; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24727
 ; LENGTH: 295
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24727

Query Match 49.0%; Score 98; DB 4; Length 295;
 Best Local Similarity 52.9%; Pred. No. 4.9e-06;
 Matches 18; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFLGLGMLGSGIVSNLLKMGHTVTWNRPTAEKCD 34
 DB 8 GFLGLGGAAMATKLVQAGLEVTWNRSAACE 41

RESULT 8
 US-09-198-452A-376
 ; Sequence 376, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 376
 ; LENGTH: 204
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-376

Query Match 42.5%; Score 85; DB 4; Length 204;
 Best Local Similarity 42.1%; Pred. No. 0.00022;
 Matches 16; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFLGLGMLGSGIVSNLLKMGHTVTWNRPTAEKCDLFQ 38
 DB 8 GLGLAWGKNVLNLMIDHGFVSQVYNTPEKTRDFLK 45

RESULT 9
 US-09-489-039A-9424
 ; Sequence 9424, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 9424
 ; LENGTH: 304
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-9424

Query Match 42.0%; Score 84; DB 4; Length 304;
 Best Local Similarity 53.0%; Pred. No. 0.0005;
 Matches 17; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

RESULT 12
US-09-252-991A-17923
; Sequence 17923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17923
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17923
Query Match 38.5%; Score 77; DB 4; Length 330;
Best Local Similarity 47.1%; Pred. No. 0.0054;
Matches 16; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy 2 FLGLGMSGGIVSNLLKMGHTVTVMNRKAEKCDL 35
Db 44 FAGLGMGVMCRRELLAAGYFLAVNRSPOKREL 77
RESULT 13
US-09-252-991A-22003
; Sequence 22003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22003
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22003
Query Match 37.5%; Score 75; DB 4; Length 221;
Best Local Similarity 57.7%; Pred. No. 0.0065;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 2 FLGLGMSGGIVSNLLKMGHTVTVMNR 27
Db 11 FLGLGNMGPPMAANLLKAGHRVNVFD 36
RESULT 14
US-09-134-001C-3241
; Sequence 3241, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13

Qy 3 LGLGLMSGGIVSNLLKMGHTVTVMNR 29
Db 23 LGLGAMGHAFASNLLKMGFTVAGWNR 49
RESULT 10
US-09-364-230-2
; Sequence 2, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (244)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)
US-09-364-230-2
Query Match 40.5%; Score 81; DB 4; Length 247;
Best Local Similarity 71.4%; Pred. No. 0.001;
Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 14 SNLLKMGHTVTVMNRKAEKCD 34
Db 2 SNLKAGCDVTVMNRKSKCD 22
RESULT 11
US-09-489-039A-9294
; Sequence 9294, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9294
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9294
Query Match 40.2%; Score 80.5; DB 4; Length 307;
Best Local Similarity 31.0%; Pred. No. 0.0016;
Matches 18; Conservative 10; Mismatches 9; Indels 21; Gaps 1;
Qy 1 GFLGLMSGGIVSNLLKMGHTVTVMNR-----AEKCDLFI 37
Db 17 GFGLGIMGKPMKSNLLKAGYSLVSDRNPEIAADVIAAGATATTTPKRAIAEQCEVII 74


```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-058-692-2

Query Match 36.5%; Score 73; DB 3;
Best Local Similarity 35.3%; Pred. No. 0.031;
Matches 12; Conservative 10; Mismatches 1

QY 1 GFLGLGMSGVISNLLKMGHTVTWNRRAEKCD 34
DB 7 GVGVMVAMGRNUALNIESRGYTVAINRSKTE 40

RESULT 17
US-09-584-628-2
; Sequence 2, Application US/09584628
; Patent No. 6309866
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: 6-phosphogluconate dehydr
; TITLE OF INVENTION: ogenase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/584,628
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-584-628-2

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Query Match 36.5%; Score 73; DB 4; Length 474;
 Best Local Similarity 35.3%; Pred. No. 0.031;
 Matches 12; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTVNRTAEKCD 34
 Db 7 GVGMAVGRNLALNIESRGYTVIYNSKEKTE 40

RESULT 18
 US-09-543-681A-5380
 ; Sequence 5380, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 5380
 ; LENGTH: 486
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-5380

Query Match 36.0%; Score 72; DB 4; Length 486;
 Best Local Similarity 34.4%; Pred. No. 0.044;
 Matches 11; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTVNRTAEK 32
 Db 25 GVGMAVGRNLALNIESRGYTVIYNSRSDK 56

RESULT 19
 US-09-252-991A-26001
 ; Sequence 26001, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 26001
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-26001

Query Match 34.5%; Score 69; DB 4; Length 324;
 Best Local Similarity 45.2%; Pred. No. 0.072;
 Matches 14; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 FLGLGLMGSGIVSNLLKMGHTVTVNRTAEK 32
 Db 42 FLGLGTMGYPMAGHLQREGYDVCVYNSRSAK 72

RESULT 20
 US-09-621-976-6407
 ; Sequence 6407, Application US/09621976
 ; Patent No. 6639063

GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 6407
 ; LENGTH: 74
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-621-976-6407

Query Match 34.0%; Score 68; DB 4; Length 74;
 Best Local Similarity 37.1%; Pred. No. 0.017;
 Matches 13; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 3 LGLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFI 37
 Db 9 IGLAVMGQNLILNNDHGFVVCANRTVSKVDDFL 43

RESULT 21
 US-09-364-230-12
 ; Sequence 12, Application US/09364230
 ; Patent No. 6348339
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; APPLICANT: Hitz, William D.
 ; APPLICANT: Kinney, Anthony J.
 ; APPLICANT: Rafalski, J. Antoni
 ; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
 ; FILE REFERENCE: BB-1178
 ; CURRENT APPLICATION NUMBER: US/09/364,230
 ; CURRENT FILING DATE: 1999-07-29
 ; EARLIER APPLICATION NUMBER: 60/094,990
 ; EARLIER FILING DATE: July 31, 1998
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 12
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (154)
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (176)
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (184)..
 US-09-364-230-12

Query Match 34.0%; Score 68; DB 4; Length 350;
 Best Local Similarity 52.0%; Pred. No. 0.11;
 Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTV 25
 Db 44 GFGLGNMGSHMARNLVRAGYRVSV 68

RESULT 22
 US-09-711-164-438
 ; Sequence 438, Application US/09711164
 ; Patent No. 6589738
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Kari

```
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29293

Query Match      32.5%; Score 65; DB 4; Length 154;
Best Local Similarity 46.2%; Pred. No. 0.11;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY   2 FLGLGMSGIVSNLLKMGHTVTWVN 27
    ||| ||| : : |||| | : : : 
DB   43 FIGLHGAGPMAINLLKAGYLLNVFD 68

RESULT 25
US-09-252-991A-27650
; Sequence 27650, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27650
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27650

Query Match      32.5%; Score 65; DB 4; Length 543;
Best Local Similarity 47.8%; Pred. No. 0.49;
Matches 11; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY   1 GFGLGLGMSGIVSNLLKMGTV 23
    ||| ||| : : ||| ||| : 
DB   252 GFIGTGIMKPQAQLNQAGHSL 274

RESULT 26
US-09-489-039A-12581
; Sequence 12581, Application US/09489039A
; Patent NO. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMOTAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12581
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12581

Query Match      32.0%; Score 64; DB 4; Length 303;
Best Local Similarity 48.0%; Pred. No. 0.34;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY   4 GLGLGMSGIVSNLLKMGHTVTWNR 28
    ||| ||| : : ||| ||| : 
DB   14 GGGLGRHLPLFLDLGHSTVSTR 38
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; ORGANISM: M.catarrhalis
US-09-540-236-2874

Query Match          31.0%; Score 62; DB 4; Length 466;
Best Local Similarity 42.3%; Pred. No. 1.1;
Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 3 LGLGLMGSGIVSNLLKMGHTVTVMNR 28
DB 244 IAGMGISTEIAEDIAKAGHQVTLNR 269

RESULT 30
US-09-134-001C-3137
; Sequence 3137, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3137
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3137

Query Match          30.5%; Score 61; DB 4; Length 352;
Best Local Similarity 32.3%; Pred. No. 1.1;
Matches 10; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 4 LGLGLMGSGIVSNLLKMGHTVTVMNR 34
DB 28 GMSFGTALANVLAQNGHDVLMGKNVND 58

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Job time : 21 secs
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RESULT 27
US-09-489-039A-10010
; Sequence 10010, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10010
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10010

Query Match          32.0%; Score 64; DB 4; Length 321;
Best Local Similarity 34.4%; Pred. No. 0.37;
Matches 11; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNR 32
DB 149 GIMGLGEIGGIADQLARLGRVSGWRSRSEKQ 180

RESULT 28
US-09-198-452A-923
; Sequence 923, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 923
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-923

Query Match          31.5%; Score 63; DB 4; Length 334;
Best Local Similarity 35.5%; Pred. No. 0.53;
Matches 11; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNR 31
DB 6 GYLGMGIWGFCLASLLANKGYPPVVAWSRNP 36

RESULT 29
US-09-540-236-2874
; Sequence 2874, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2874
; LENGTH: 466
; TYPE: PRT
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:45:18 ; Search time 48 Seconds
(without alignments)

254.231 Million cell updates/sec

Title: US-10-067-482-2_COPY_271_308

Perfect score: 200

Sequence: 1 GFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFTQ 38

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Total number of hits satisfying chosen parameters: 1342398

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	200	100.0	553	14	US-10-067-482-2
2	166	83.0	547	14	US-10-067-482-3
3	166	83.0	550	14	US-10-103-313-417
4	164	82.0	276	14	US-10-067-482-4
5	125	62.5	289	14	US-10-167-547C-16
6	124	62.0	333	12	US-10-424-599-144794
7	121	60.5	176	16	US-10-767-701-60840
8	121	60.5	343	16	US-10-437-963-116017
9	118	59.0	290	14	US-10-167-547C-14
10	118	59.0	293	16	US-10-437-963-174476
11	117	58.5	81	16	US-10-767-701-52389
12	117	58.5	364	12	US-10-425-114-50561
13	109	54.5	292	12	US-10-282-122A-52083
14	106	53.0	288	12	US-10-282-122A-45255
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Sequence 12590, A
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Sequence 61555, A
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Sequence 55145, A
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Sequence 256, App
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ALIGNMENTS

Query Match	100.0%;	Score 200;	DB 14;	Length 553;
Best Local Similarity	100.0%;	Pred. No. 2.7e-19;		
Matched 30	Conservative	0.	Mismatches 0;	Indels 0;
Matched 0	Conservative	0.	Mismatches 0;	Indels 0;
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RESULT 3
US-10-103-313-417

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Query Match      83.0%; Score 166; DB 14; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-10-067-482-4
; Sequence 4, Application US/10067482
; Publication No. US20030148407A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies, Inc.
; TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
; FILE REFERENCE: 1U 102 R1
; CURRENT APPLICATION NUMBER: US/10/067,482
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 276
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-4

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Query Match      82.0%; Score 164; DB 14; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 8 MGSGIVSNLLKMGHTVTWNR~~TAEKCDLFIQ~~ 38
|||||
Dh 1 MGSGIVSNLLKMGHTVTWNR~~TAEKCDLFIQ~~ 31
|||||

RESULT 5
US-10-167-547C-16
Sequence 16, Application US/10167547C
Publication No. US20030170653A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/297198
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 16
LENGTH: 289
TYPE: PRT
ORGANISM: Arabidopsis

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Query Match      60.5%; Score 121; DB 16; Length 176;
Best Local Similarity 64.7%; Pred. NO.8.5e-09;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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RESULT 10
US-10-437-963-174476
; Sequence 174476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

Query Match 54.5%; Score 109; DB 12; Length 292;
Best Local Similarity 62.5%; Pred. No. 7.3e-07;
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFLGLMGSGIVSNLLKMGHTVTVNRTAEK 32
|||:|||:|||:|||:|||:|||:|||:
Db 9 GFIGTGVMGKGMIKNLLKGGYTVHVYNRTKEK 40

RESULT 14

US-10-282-122A-45255
 ; Sequence 45255, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.

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; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
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; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45255
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; JUS-10-282-122A-45255

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Query Match 53.0%; Score 106; DB 12; Length 288;
Best Local Similarity 55.6%; Pred. No. 1.9e-06;
Matches 20; Conservative 5; Mismatches 11; Indels

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US-10-282-122A-44990
Sequence 44990, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:

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? APPLICANT: Wang, Liangsu
? APPLICANT: Zamudio, Carlos
? APPLICANT: Malone, Cheryl
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlsen, Kari
? APPLICANT: Zyskind, Judith
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John
? APPLICANT: Carr, Grant
? APPLICANT: Yamamoto, Robert
? APPLICANT: Forsyth, R.
? APPLICANT: Xu, H.
? TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
? FILE REFERENCE: EUIPA 034A
? CURRENT APPLICATION NUMBER: US/10/282,122A
? CURRENT FILING DATE: 2003-02-20
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/230,335
? PRIOR FILING DATE: 2000-09-06
? PRIOR APPLICATION NUMBER: 60/230,347
? PRIOR FILING DATE: 2000-09-09
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/267,636
? PRIOR FILING DATE: 2001-02-09
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 78614
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 44990
? LENGTH: 290
? TYPE: PRT
? ORGANISM: Acinetobacter baumannii
US-10-282-122A-44990

```

```
Query Match          52.5%; Score 105; DB 12; Length 290;
Best Local Similarity 59.4%; Pred. No. 2.6e-06;
Matches 19; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
```

Qy 1 GFLGLMGSGIVSNLLKMGHTVTVNRTAEK 32
||| : ||| : ||| | | | | | : |
Dd 5 GFVGTGIMGMPMANLLKAGHQVKVNRTSSK 36

RESULT 16

US-10-282-122A-57891
; Sequence 57891, Application US/10282122A
; Publication No. US20040029129A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identificatio
/ FILE REFERENCE: EUIPA-034A

```

```

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57891
LENGTH: 295
TYPE: PRT
ORGANISM: Enterococcus faecium
US-10-282-122A-57891

Query Match          50.0%; Score 100; DB 12; Length 295;
Best Local Similarity 52.9%; Pred. No. 1.3e-05;
Matches 18; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCD 34
        |||:|||||:::||:|||||
Db       4  GFIGTGVMSAVARHLLERAGHEVAVYNRTAKAD 37

RESULT 17
US-10-369-493-11979
Sequence 11979, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052/B)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11979
LENGTH: 475
TYPE: PRT
ORGANISM: Mesorhizobium loti
US-10-369-493-11979

Query Match          48.0%; Score 96; DB 15; Length 475;
Best Local Similarity 42.1%; Pred. No. 8.4e-05;
Matches 16; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      1  GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38
        |||:|||||:::||:|||||
Db       7  GLIGLTGMSNALTAEHGHRIAFVNRTARTDAFVE 44

```

```

Best Local Similarity   42.1%;    Pred. No. 0.0011;
Matches      16; Conservative     9; Mismatches   13; Indels

QY      1 GFLGLGMLSGIVSNLLKMGHTVTWNRTAEKCDLFIQ 38
       |||:|||||:|:|||||||:|:|||||:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db       4 GIYGVLGWGSNLIANIADGNFNSVYNRDNEKTEIFVK 41
          |::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 21
US-09-815-242-5781
; Sequence 5781, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5781
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5781

Query Match           44.0%;    Score 88; DB 9; Length 465;
Best Local Similarity 39.5%;    Pred. No. 0.0011;
Matches      15; Conservative    12; Mismatches   11; Indels

QY      1 GFLGLGMLSGIVSNLLKMGHTVTWNRTAEKCDLFIQ 38
       |||:|||||:|:|||||||:|:|||||:|:|||||:~
Db       4 GVIGLAVMKGNLAWNIERGYSVSVFNESSEKTDLMVE 41
          |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 22
US-09-815-242-12590
; Sequence 12590, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A Prokaryotes
```

```

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 12590
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12590

Query Match      44.0%; Score 88; DB 9; Length 468;
Best Local Similarity 39.5%; Pred. No. 0.0011;
Matches 15; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGMSGGIVSNLLKMGHTVTWNRATKCDLFIQ 38
Db 6 GVIGLAVMGKNLAWNIESRGYSVFNRSSEKTLWVE 43

RESULT 23
US-10-369-493-2943
; Sequence 2943, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiaofeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2943
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-369-493-2943

Query Match      44.0%; Score 88; DB 15; Length 469;
Best Local Similarity 36.8%; Pred. No. 0.0011;
Matches 14; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGMSGGIVSNLLKMGHTVTWNRATKCDLFIQ 38
Db 6 GLIGLAVMGONLAINIARKYKSVNRYNRTAQTDFEVK 43

RESULT 24
US-10-424-599-258895
; Sequence 258895, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258895
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75806C.1.pep
US-10-424-599-258895

Query Match      43.5%; Score 87; DB 12; Length 122;
Best Local Similarity 40.5%; Pred. No. 0.00033;
Matches 15; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFLGLGMSGGIVSNLLKMGHTVTWNRATKCDLFI 37
Db 22 GLIGLGVGNSLAINIAEKGNRIAVFNRTPARTDFEL 58

RESULT 25
US-10-282-122A-43907
; Sequence 43907, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43907
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

```

US-10-282-122A-43907

Query Match	43.5%;	Score 87;	DB 12;	Length 468;
Best Local Similarity	39.5%;	Pred. No. 0.0015;		
Matches 15; Conservative	12;	Mismatches 11;	Indels	

Qy 1 GFLGLMGSGIVSNLLKMGHTVTYVNRRTAEKCDLFQ 38
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 6 GVIGLAVMGKNLANWNITESHGYSVSVPNRSSEKTDLMVE 43

RESULT 26

```

US-10-686-736-3
; Sequence 3, Application US/10686736
; Publication NO. US20040063181A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; FILE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/686,736
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/10/078,167A
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

```

Query Match 43.0%; Score 86; DB 12; Length 459;
Best Local Similarity 43.2%; Pred. No. 0.002;
Matches 16; Conservative 8; Mismatches 13; Indels

1 GFGLGLMGSGIVSNLLKMGHTVTWVNRTEAKCDLFI 37
19 GVYGLAVMGSLNARNGFNGTVAVYNRTDKTDKLI 55

RESULT 27

```

US-10-078-167-3
; Sequence 3, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockett, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; FILE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/078, 167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-078-167-3

```

Query Match 43.0%; Score 86; DB 14; Length 459;
Best Local Similarity 43.2%; Pred. No. 0.002;
Matches 16; Conservative 8; Mismatches 13; Indels

1 GFLGLMGSGIVSNLLKMGHTVTVWNRRTAEKCDLFI 37

Db 19 GVGLAVMGSLARNFARNGNTVAVYNRSTDKTDKLI 55

RESULT 28

US-10-282-122A-60359
; Sequence 60359, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

APPLICANT:	Wang, Liangsu
APPLICANT:	Zamudio, Carlos
APPLICANT:	Malone, Cheryl
APPLICANT:	Haselbeck, Robert
APPLICANT:	Ohlsen, Kari
APPLICANT:	Zyskind, Judith
APPLICANT:	Wail, Daniel
APPLICANT:	Trawick, John
APPLICANT:	Carr, Grant
APPLICANT:	Yamamoto, Robert
APPLICANT:	Forsyth, R.
APPLICANT:	Xu, H.

```

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60359
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-10-282-122A-60359

```

Query Match 43.0%; Score 86; DB 12; Length 472;
Best Local Similarity 43.8%; Pred. No. 0.0021;
Matches 14; Conservative 9; Mismatches 9; Indels

Qy 1 GFLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
| : | : | : | : | : | : | : | : | :
Dd 7 GVIGMGMGRNLALNIESRGHTVSIENRSTEK 38

RESULT 29

```

US-09-738-626-5105
; Sequence 5105, Application US/09738626
; Publication NO. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO

```

Thu Sep 16 09:36:50 2004

```

; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5105
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5105

Query Match          43.0%; Score 86; DB 9; Length 492;
Best Local Similarity 43.2%; Pred. No. 0.0022;
Matches 16; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY      1  GFLGLMGSGIVSNLLKMGHTVTVMNRRTAEKCDLFI 37
        |::|::|::|::|::|::|::|::|::|::|::|::|
DB      19  GVGGLAVMGSLARNFARNGTIVAVVNRSTDKTKLI 55

RESULT 30
US-10-767-701-61555
; Sequence 61555, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 61555
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 9847593.pep
US-10-767-701-61555

Query Match          42.5%; Score 85; DB 16; Length 154;
Best Local Similarity 40.5%; Pred. No. 0.00081;
Matches 15; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      1  GFLGLMGSGIVSNLLKMGHTVTVMNRRTAEKCDLFI 37
        |::|::|::|::|::|::|::|::|::|::|::|::|
DB      26  GWIGIGVWGGAAGVTVAYARTPTSKAGFV 62

Search completed: September 16, 2004, 07:47:49
Job time : 51 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:32:13 ; Search time 15 Seconds
(without alignments)

243.685 Million cell updates/sec

Title: US-10-067-482-2_COPY_271_308

Perfect score: 200

Sequence: 1 GFLGLMGSGIVSNLLKMGHTVWNRFAEKDLEFIQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_78:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	54.5	292	2	G97310
2	108	54.0	289	2	dehydrogenase rela
3	99	49.5	288	2	oxidoeductase [im
4	98	49.0	291	2	3-hydroxyisobutyra
5	92	46.0	334	2	probable dehydroge
6	90	45.0	293	2	hypothetical prote
7	90	45.0	293	2	probable D-threoni
8	88	44.0	464	2	phosphogluconate d
9	88	44.0	464	2	phosphogluconate d
10	88	44.0	469	2	6-phosphogluconate d
11	86	43.0	286	2	3-hydroxyisobutyra
12	86	43.0	472	2	phosphogluconate d
13	86	43.0	472	2	phosphogluconate d
14	85	42.5	479	2	6-phosphogluconate
15	85	42.5	479	2	6-phosphogluconate
16	85	42.5	479	2	6-phosphogluconate
17	84.5	42.2	299	1	6-phosphogluconate
18	84.5	42.2	299	1	3-hydroxyisobutyra
19	84.5	42.2	299	2	probable dehydroge
20	84	42.0	288	2	probable dehydroge
21	84	42.0	295	2	3-hydroxyisobutyra
22	84	42.0	299	2	probable dehydroge
23	84	42.0	299	2	probable dehydroge
24	83	41.5	468	2	probable phosphogl
25	82.5	41.2	291	2	phosphogluconate d
26	82.5	41.2	294	2	3-hydroxyisobutyra
27	82	41.0	293	2	2-hydroxy-3-oxopro
28	82	41.0	297	2	hypothetical prote
29	82	41.0	300	2	probable dehydroge
					oxidoeductase [imp

30	82	41.0	300	2	C97687	D-threonine dehydr
31	81	40.5	286	2	AE1200	3-hydroxyisobutyra
32	81	40.5	467	2	JC2306	phosphogluconate d
33	81	40.5	476	2	AE2764	phosphogluconate d
34	81	40.5	476	2	D97545	6-phosphogluconate
35	80	40.0	289	2	H90248	3-hydroxyisobutyra
36	80	40.0	298	2	E91229	probable dehydroge
37	80	40.0	288	2	D86076	probable dehydroge
38	80	40.0	298	2	S40826	hypothetical 31.2K
39	80	40.0	298	2	AI0947	hypothetical 31.2K
40	80	40.0	476	2	AC2465	probable oxidoeduct
41	80	40.0	476	2	AC2465	6-phosphogluconate
42	80	40.0	479	2	A8565	phosphogluconate d
43	80	40.0	484	2	C64077	phosphogluconate d
44	80	40.0	485	2	D70664	phosphogluconate d
45	79	39.5	492	2	S64588	probable gnd prote
46	79	39.5	469	2	AC3650	phosphogluconate d
47	79	39.5	480	2	A71561	phosphogluconate d
48	79	39.5	483	2	JE0234	probable 6-phospho
49	77	38.5	489	1	S46671	phosphogluconate d
50	77	38.5	296	2	C83232	phosphogluconate d
51	77	38.5	315	2	H82512	probable 3-hydroxy
52	77	38.5	482	2	T01659	phosphogluconate d
53	77	38.5	484	2	JC5282	phosphogluconate d
54	76	38.0	226	2	T01658	phosphogluconate d
55	76	38.0	286	2	S76263	phosphogluconate d
56	76	38.0	482	2	E87444	hypothetical prote
57	76	38.0	482	2	C82404	conserved hypothet
58	76	38.0	483	2	D87167	6-phosphogluconate
59	75	37.5	486	2	T44750	probable phosphogl
60	75	37.5	298	1	C42902	3-hydroxyisobutyra
61	75	37.5	371	2	T10635	3-hydroxyisobutyra
62	74	37.0	482	2	E81248	6-phosphogluconate
63	74	37.0	125	2	H47677	hypothetical prote
64	74	37.0	296	2	T34859	probable dehydroge
65	74	37.0	315	2	A98338	D-threonin dehydro
66	74	37.0	468	1	AI2944	3-hydroxyisobutyra
67	74	37.0	468	2	S04397	phosphogluconate d
68	74	37.0	468	2	I62463	phosphogluconate d
69	74	37.0	468	2	D56146	phosphogluconate d
70	74	37.0	468	2	I84555	phosphogluconate d
71	74	37.0	468	2	I41250	phosphogluconate d
72	74	37.0	468	2	AE0765	phosphogluconate d
73	74	37.0	492	2	T40628	6-phosphogluconate
74	74	37.0	508	2	T42523	probable phosphogl
75	73	36.5	511	2	T05363	phosphogluconate d
76	73	36.5	287	2	E72666	probable 3-hydroxy
77	73	36.5	290	2	S76381	probable 3-hydroxy
78	73	36.5	443	2	I40708	phosphogluconate d
79	73	36.5	468	1	DEECGC	phosphogluconate d
80	73	36.5	468	2	I62465	phosphogluconate d
81	73	36.5	468	2	I41249	phosphogluconate d
82	73	36.5	468	2	F90982	gluconate-6-phosph
83	73	36.5	468	2	D85828	gluconate-6-phosph
84	73	36.5	472	2	F86702	gluconate-6-phosph
85	73	36.5	474	2	E95043	hypothetical prote
86	73	36.5	474	2	G97913	hypothetical prote
87	72	36.0	482	2	B82021	phosphogluconate d
88	72	36.0	211	2	AC2560	phosphogluconate d
89	72	36.0	469	2	AI0187	hypothetical prote
90	71	35.5	486	2	S57786	phosphogluconate d
91	70	35.0	356	2	E71252	phosphogluconate d
92	70	35.0	292	2	AB0567	probable glycerol -
93	70	35.0	298	2	C96022	2-hydroxy-3-oxopro
94	69	34.5	310	2	AB3338	probable 3-hydroxy
95	69	34.5	285	2	G71912	3-hydroxyisobutyra
96	69	34.5	288	2	F83447	probable 3-hydroxy
97	69	34.5	297	2	D91027	probable sugar nuc
98	69	34.5	297	2	E85871	probable sugar nuc
99	68	34.0	289	2	A32867	3-hydroxyisobutyra
100	68	34.0	289	2	B81065	3-hydroxyacid dehy
			289	2	B81802	hypothetical prote

ALIGNMENTS

RESULT 1
G97310
dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC B. subtilis ortholog
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C/Accession: G97310
R.Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G97310
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-292 <KUR>
A/Cross-references: GB:AB001437; PIDN:AAK81274.1; PID:gl5026424; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC3342
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom

Query Match 54.5%; Score 109; DB 2; Length 292;
Best Local Similarity 62.5%; Pred. No. 4.3e-07;
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRTEAK 32
DB 9 GFITGTVMGKMTKLNLLKGGYTVHVNRTEK 40

RESULT 2
G90314
oxidoreductase [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C/Accession: G90314
R. She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrest, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: G90314
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-289 <KUR>
A/Cross-references: GB:AE006641; NID:gl3814790; PIDN:AAK41774.1; GSPDB:GN00155
A/Genetics:
A/Gene: SS01560
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 54.0%; Score 108; DB 2; Length 289;
Best Local Similarity 58.8%; Pred. No. 5.8e-07;
Matches 20; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRTEAKCD 34
DB 4 GFILGILGMPFASNLLKAGYDLTVYNRTIEKAE 37

RESULT 3
B69870
3-hydroxyisobutyrate dehydrogenase homolog yKWC - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C/Accession: B69870
R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togonoi, A.; Tozato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:198044033; PMID:9384377
A/Accession: B69870
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-288 <KUN>
A/Cross-references: GB:Z99111; GB:AL009126; NID:G2633699; PIDN:CAB13269.1; PID:G2633767
A/Experimental source: strain 168
C/Genetics:
A/Gene: yKwc
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
F; 5-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HID>

Query Match 49.5%; Score 99; DB 2; Length 288;
Best Local Similarity 47.4%; Pred. No. 9.6e-06;
Matches 18; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFILGLGMSGIVSNLLKMGHTVTVMNRTEAKCDLFQ 38
DB 6 GFILGLGMSKMSASHLNDGHPVLVYTRTEKAEISLQ 43

RESULT 4
D83371
probable dehydrogenase PA2199 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Nov-2001
C/Accession: D83371
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: D83371
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-291 <STO>
A/Cross-references: GB:AE004646; GB:AE004091; NID:G9948213; PIDN:AG05587.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA2199
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 49.0%; Score 98; DB 2; Length 291;
Best Local Similarity 52.9%; Pred. No. 1.3e-05;
Matches 18; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRTEAKCD 34
DB 4 GFLGLGMSGAATRLVQAGLEVTVNRSAAACE 37

RESULT 5
T08967
hypochemical protein, Fl9B15.150 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2000
C/Accession: T08967
R. Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16519
A/Accession: T08967

A:Molecule type: DNA

A:Residues: 1-334 <BEV>

A:Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150

A:Experimental source: cultivar Columbia; BAC clone F19B15

C:Genetics:

A:Gene: ATSP:F19B15.150

A:Map position: 4

C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase homolog <HIB>
F:40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homolog <HIB>

Query Match 46.0%; Score 92; DB 2; Length 334;
Best Local Similarity 45.9%; Pred. No. 0.0001;
Matches 17; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTWNRATAKCDLFI 37

DB 41 GWIGTVMGSRMCGHLIRAGYTVTVNRTSKAQTLI 77

RESULT 6

G95277

Probable D-threonine [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymA
C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: G95277

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: G95277

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-293 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK64785.1; PID:g14523194; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasamid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMA0237

A:Genome: plasmid

C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase homolog

Query Match 45.0%; Score 90; DB 2; Length 293;

Best Local Similarity 54.5%; Pred. No. 0.00016;

Matches 18; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 FLGLGLMSGIVSNLLKMGHTVTWNRATAKCD 34

DB 9 FLCTGLMGAPMARLLGAGFVTVNRDAKAE 41

RESULT 7

S14628

phosphoglucuronate dehydrogenase (decarboxylating) (EC 1.1.1.44) - Synecococcus sp.

C:Species: Synecococcus sp.

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S14628

R:Culler, D.C.; Krogmann, D.W.

A:Description: Amino acid sequence comparisons of 6-Phosphoglucuronate Dehydrogenase.

A:Reference number: S14628

A:Accession: S14628

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-470 <CUL>

A:Cross-references: EMBL:X58719; NID:947524; PIDN:CAA41555.1; PID:g47525

C:Superfamily: phosphoglucuronate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

C:Keywords: oxidoreductase; pentose phosphate pathway

F:6-288/Domain: 3-hydroxyisobutyrate dehydrogenase homolog <HIB>

Query Match 45.0%; Score 90; DB 1; Length 470;

Best Local Similarity 43.2%; Pred. No. 0.00027;

Matches 16; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGLMSGIVSNLLKMGHTVTWNRATAKCDLFI 37

DB 7 GLIGLAVMGENLALNIERNFSLTYNRTAEKTEAFM 43

RESULT 8

H70169

phosphoglucuronate dehydrogenase, decarboxylating (gnd) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jun-1999

C:Accession: H70169

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: H70169

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-464 <KLE>

A:Cross-references: GB:AE001157; GB:AE000783; NID:g2688471; PIDN:AAK66918.1; PID:g2688472

A:Experimental source: strain B31

C:Superfamily: phosphoglucuronate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

F:3-280/Domain: 3-hydroxyisobutyrate dehydrogenase homolog <HIB>

Query Match 44.0%; Score 88; DB 2; Length 464;

Best Local Similarity 42.1%; Pred. No. 0.0005;

Matches 16; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLGLMSGIVSNLLKMGHTVTWNRATAKCDLFIQ 38

DB 4 GYGLGVMGSLNALNIADNGFNVINRDNEKTEIFVK 41

RESULT 9

G89930

phosphoglucuronate dehydrogenase [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: G89930

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; H
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: G89930

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-468 <KUR>

A:Cross-references: GB:BA000018; PID:g13701310; PIDN:BAK42604.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: gnd

C:Superfamily: phosphoglucuronate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

Query Match 44.0%; Score 88; DB 2; Length 468;

Best Local Similarity 39.5%; Pred. No. 0.00051;

Matches 15; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGLMSGIVSNLLKMGHTVTWNRATAKCDLFIQ 38

DB 1 GFLGLGLMSGIVSNLLKMGHTVTWNRATAKCDLFIQ 38

```
Db      6  GVIGLAVMGKNLAWNIESRGYSVFNRSSEKTDLMVE 43

RESULT 10
A72377
6-phosphogluconate dehydrogenase, decarboxylating - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: A72377
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: A72377
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-469 <ARN>
A/Cross-references: GB:AB001722; GB:AE000512; NID:g4980938; PIDN:AAD35523.1; PID:g498094
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM0438
C/Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;5-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match      44.0%; Score 88; DB 2; Length 469;
Best Local Similarity 36.8%; Pred. No. 0.00051;
Matches 14; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AC1558
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1558
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:g16413463; GSPDB:GN00178
A/Experimental source: strain Clp11262
C/Genetics:
A/Gene: lin1004
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match      43.0%; Score 86; DB 2; Length 286;
Best Local Similarity 40.5%; Pred. No. 0.00059;
Matches 15; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

C/Species: Listeria innocua
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C/Accession: F86535
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ts
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: F86535
A/Status: preliminary

RESULT 12
AD1609
6-phosphogluconate dehydrogenase homolog lin1413 [imported] - Listeria innocua (strain C
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

Db      6  GVIGLAVMGKNLAWNIESRGYSVFNRSSEKTDLMVE 43

RESULT 10
A72377
6-phosphogluconate dehydrogenase, decarboxylating - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: A72377
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: A72377
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-469 <ARN>
A/Cross-references: GB:AB001722; GB:AE000512; NID:g4980938; PIDN:AAD35523.1; PID:g498094
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM0438
C/Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;5-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match      44.0%; Score 88; DB 2; Length 469;
Best Local Similarity 36.8%; Pred. No. 0.00051;
Matches 14; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AC1558
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1558
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:g16413463; GSPDB:GN00178
A/Experimental source: strain Clp11262
C/Genetics:
A/Gene: lin1004
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match      43.0%; Score 86; DB 2; Length 286;
Best Local Similarity 40.5%; Pred. No. 0.00059;
Matches 15; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

C/Species: Listeria innocua
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C/Accession: F86535
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ts
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: F86535
A/Status: preliminary

RESULT 13
AH1246
6-phosphogluconate dehydrogenase homolog lmo1376 [imported] - Listeria monocytogenes (st
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AH1246
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AH1246
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-472 <GLA>
A/Cross-references: GB:NC_003210; PIDN:CAC99454.1; PID:g16410792; GSPDB:GN00177
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: lmo1376
C/Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

Query Match      43.0%; Score 86; DB 2; Length 472;
Best Local Similarity 43.8%; Pred. No. 0.00095;
Matches 14; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

C/Species: Chlamydia pneumoniae [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C/Accession: F86535
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ts
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: F86535
A/Status: preliminary
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A:Molecule type: DNA
A:Residues: 1-479 <STO>
A:CROSS-references: GB:BA000008; NID:g8978732; PIDN:BAA98568.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: gnd
C:Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

Query Match 42.5%; Score 85; DB 2; Length 479;
Best Local Similarity 42.1%; Pred. No. 0.0013;
Matches 16; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFGLGILMGSGIVSNLLKMGHTVTVMNRTPAEKCDFIQ 38
| : | : | : | : | : | : | : | : | : | : | :
Db 6 GLIGLAVMGKNLVLMNMIDHGFSSVYNRTPEKTRDFLK 43

RESULT 15
C72088
6-phosphoglucuronate dehydrogenase, decarboxylating CP0398 [imported] - Chlamydia pneumoniae
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: C72088; H81581
R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72088
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <ARN>
A:CROSS-references: GB:AE001620; GB:AE001363; NID:g4376631; PIDN:AAD18504.1; PID:g437663
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: H81581
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <REA>
A:CROSS-references: GB:AE002201; GB:AE002161; NID:g7189316; PIDN:AAF38243.1; PID:g718932
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: gnd; CP0398
C:Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

F 5-284/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match 42.5%; Score 85; DB 2; Length 479;
Best Local Similarity 42.1%; Pred. No. 0.0013;
Matches 16; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFGLGILMGSGIVSNLLKMGHTVTVMNRTPAEKCDFIQ 38
| : | : | : | : | : | : | : | : | : | : | :
Db 6 GLIGLAVMGKNLVLMNMIDHGFSSVYNRTPEKTRDFLK 43

RESULT 16
AB1714
6-phosphoglucuronate dehydrogenase, decarboxylating TC0333 [imported] - Chlamydia muridarum
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 28-Jul-2000
C:Accession: AB1714
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: AB1714
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <TET>

Thu Sep 16 09:36:51 2004

us-10-067-482-2_copy_271_308.rpr

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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4003
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
Query Match 42.2%; Score 84.5; DB 2; Length 299;
Best Local Similarity 32.8%; Pred. No. 0.00092;
Matches 19; Conservative 9; Mismatches 9; Indels 21; Gaps 1;
QY 1 GFLGLGMSGIVSNLLKMGHTVTWNRT-----AEKCDLFI 37
Db 9 GFGLGIMGKPMKXNLLKAGISLVVADRNPEAIADVIAAGTAETASTAKAIAEQCDVII 65

RESULT 19
C85974
probable dehydrogenase yhaB [imported] - Escherichia coli (strain O157:H7, substrain EDL
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C85974
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85974
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <STO>
A;Cross-references: GB:AE005174; NID:g12517718; PIDN:AAG58255.1; GSPDB:GN00145; UMG:Z44
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yhaB
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
Query Match 42.2%; Score 84.5; DB 2; Length 299;
Best Local Similarity 32.8%; Pred. No. 0.00092;
Matches 19; Conservative 9; Mismatches 9; Indels 21; Gaps 1;
QY 1 GFLGLGMSGIVSNLLKMGHTVTWNRT-----AEKCDLFI 37
Db 9 GFGLGIMGKPMKXNLLKAGISLVVADRNPEAIADVIAAGTAETASTAKAIAEQCDVII 66

RESULT 20
C70303
3-hydroxyisobutyrate dehydrogenase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: C70303
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V,
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: C70303
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-288 <QF>
A;Cross-references: GB:AE000670; NID:g2982779; PIDN:AAC06408.1; PID:g2982783; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: hbbD
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
F;3-265/Domain: 3-hydroxyisobutyrate dehydrogenase homology <hib>
Query Match 42.0%; Score 84; DB 2; Length 288;
Best Local Similarity 44.4%; Pred. No. 0.001;
Matches 16; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 1 GFLGLGMSGIVSNLLKMGHTVTWNRTAEKCDLF 36
Db 4 GFGLGHLGRAIAKLEIQGVBLIWNRTLSKAHEF 39

```

RESULT 21

```

A96019
probable dehydrogenase protein [imported] - Sinorhizobium meliloti (strain 1021) megapla
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: A96019
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: A96019
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49817.1; PID:g15141305; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smb20710
A;Genome: plasmid
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
Query Match 42.0%; Score 84; DB 2; Length 295;
Best Local Similarity 33.9%; Pred. No. 0.0011;
Matches 20; Conservative 8; Mismatches 9; Indels 22; Gaps 2;
QY 1 GFLGLGMSGIVSNLLKMGHTVTWN---NRT-----AEKCDLFI 37
Db 7 GFGLGLMGQGAANILKKGWPLQVNAHNRPAVEMLVAGAREAKTPREMAEQCDIV 65

RESULT 22
D96736
probable dehydrogenase F23N20.16 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: D96736
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <STO>
A;Cross-references: GB:AE005173; NID:g6714325; PIDN:AAF26018.1; GSPDB:GN00141
C;Genetics:
A;Gene: F23N20.16
A;Map position: 1
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
Query Match 42.0%; Score 84; DB 2; Length 299;
Best Local Similarity 46.9%; Pred. No. 0.0011;
Matches 15; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
QY 1 GFLGLGMSGIVSNLLKMGHTVTWNRTAEK 32

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Query Match 41.2%; Score 82.5; DB 2; Length 294;

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Matches 19; Conservative 8; Mismatches 10; Indels 21; Gaps 1;
QY 1 GFLGLMGSGIVSNLLKMGHTVTVMNRT-----AEKCDLFI 37
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:
Db 4 GFTGLMGKPMKSNLLKAGSVLWSDRNPALADVIAAGAETASTAKAIAEQCDALII 61
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:

RESULT 27
G86901
hypothetical protein ywjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86901
R;Bolotin, A.; Wincker, P.; Mauer, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 <STO>
A;Cross-references: GB:AE005176; PID:gl2725281; PIDN:AAK06313.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ywjF
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 41.0%; Score 82; DB 2; Length 293;
Best Local Similarity 42.4%; Pred. No. 0.002;
Matches 14; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 2 FLGLMGSGIVSNLLKMGHTVTVMNRTAEKCD 34
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:
Db 6 FTGTGVAAGAWAGHLMADGHDLIVNRTKSKTD 38
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:

RESULT 28
E96736
probable dehydrogenase F23N20.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E96736
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
C;Accession: E96736
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: GB:AE005173; NID:96714326; PIDN:AAF26019.1; GSPDB:GN00141
C;Genetics:
A;Gene: F23N20.17
A;Map position: 1
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 41.0%; Score 82; DB 2; Length 297;
Best Local Similarity 43.8%; Pred. No. 0.002;
Matches 14; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 GFLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:
Db 17 GWIGIGMSAWSHIIAGYGVTVYVARDLRK 48
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:

RESULT 29
```

```
AH29112
oxidoreductase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2912
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43718.1; PID:gl17741249; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2737
A;Map position: circular chromosome
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 41.0%; Score 82; DB 2; Length 300;
Best Local Similarity 41.7%; Pred. No. 0.002;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY 2 FLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFI 37
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:
Db 14 FTGTGLMGPMARRLLGTGFSVKVWNRNSVDKAQALV 49
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:

RESULT 30
C97687
D-threonine dehydrogenase (AB015439) [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: C97687
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97687
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK8452.1; PID:gl5157953; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 4961
A;Map position: circular chromosome
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho

Query Match 41.0%; Score 82; DB 2; Length 300;
Best Local Similarity 41.7%; Pred. No. 0.002;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY 2 FLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFI 37
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:
Db 14 FTGTGLMGPMARRLLGTGFSVKVWNRNSVDKAQALV 49
||:||||: ||:||||: ||:||||: ||:||||: ||:||||:

Search completed: September 16, 2004, 07:46:30
Job time : 16 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:31:17 ; Search time 10 Seconds

(without alignments)
197.867 Million cell updates/sec

Title: US-10-067-482-2_COPY_271_308

Perfect score: 200

Sequence: 1 GFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	49.5	288	1 YKWC_BACSU	O34948 bacillus su
2	90	45.0	470	1 6PGD_SYN7	P21577 synechococ
3	89	44.5	517	1 6PGD_CANAL	O13287 candida alb
4	88	44.0	468	1 6PGD_STAAN	Q99272 staphylococ
5	87	43.5	324	1 D3HI_DROME	Q998m5 drosophila
6	87	43.5	468	1 6PGD_STAAM	Q911r3 staphylococ
7	85	42.5	479	1 6PGD_CHLMU	Q9pkx7 chlamydia m
8	85	42.5	479	1 6PGD_CHLPN	Q928i3 chlamydia p
9	84.5	42.2	294	1 GARR_ECOLI	P23523 escherichia
10	84	42.0	488	1 6PGD_TREPA	O83351 treponema p
11	83	41.5	468	1 6PGD_BACSU	P53174 haemophilus
12	81	40.5	467	1 6PGD_BACLI	P12013 bacillus su
13	80	40.0	298	1 YIHU_ECOLI	P52207 bacillus li
14	80	40.0	298	1 YIHU_SALTY	P32142 escherichia
15	80	40.0	479	1 6PGD_TRYBB	Q91780 salmonella
16	80	40.0	484	1 6PGD_HAEIN	P31072 trypanosoma
17	80	40.0	492	1 6PG2_YEAST	P43774 haemophilus
18	79	39.5	468	1 6PG2_BACSU	P53119 saccharomy
19	79	39.5	480	1 6PGD_CHLTR	P08059 bacillus su
20	79	39.5	489	1 6PG1_YEAST	O84066 chlamydia t
21	77	38.5	484	1 6PGD_ACTAC	P38720 saccharomy
22	75	37.5	298	1 MMSB_PSEAE	P70718 actinobacil
23	75	37.5	347	1 D3HI_ARATH	P28811 pseudomonas
24	75	37.5	468	1 6PGD_STAEP	Q8uc0 arabidopsis
25	75	37.5	485	1 6PGD_CUNEL	O60037 staphylococ
26	74	37.0	468	1 6PG9_ECOLI	P37754 escherichia
27	74	37.0	468	1 6PGD_KLEPN	P14576 klebsiella
28	74	37.0	468	1 6PGD_SALTY	P14062 salmonella
29	74	37.0	481	1 6PGD_CERCA	P41570 ceratitis c
30	74	37.0	481	1 6PGD_SCHPO	P78812 schizosacch
31	73	36.5	290	1 Y229_SYNV3	Q55702 synechocyst
32	73	36.5	468	1 6PGD_ECOLI	P00350 escherichia
33	73	36.5	468	1 6PGD_SHIFL	P37756 shigella fl

34	73	36.5	472	1 6PGD_LACLA	Q3chu6 lactococcus
35	73	36.5	472	1 6PGD_LACLC	P96789 lactococcus
36	72	36.0	336	1 D3HI_HUMAN	P31937 homo sapien
37	71	35.5	356	1 6PDA_TREPA	O83973 treponema p
38	69	34.5	335	1 D3HI_RAT	P29266 rattus norv
39	69	34.5	335	1 D3HI_MOUSE	Q99113 mus musculu
40	68	34.0	332	1 6PGD_CLOAB	Q971d6 clostridium
41	68	34.0	482	1 6PGD_HUMAN	P52209 mus sapien
42	68	34.0	482	1 6PGD_MOUSE	Q9cdc0 mus musculu
43	68	34.0	482	1 6PGD_SHEEP	P00349 ovis aries
44	67	33.5	292	1 GLXR_ECOLI	P77161 escherichia
45	67	33.5	292	1 YFCH_ECOLI	P77775 escherichia
46	66.5	33.2	281	1 HBD_CLODI	P45364 clostridium
47	66	33.0	35	1 D3HI_RABIT	F32185 oryctolagus
48	66	33.0	482	1 6PGD_SINY3	P52208 synechocyst
49	64	32.0	299	1 DH31_CABEL	Q9xt10 caenorhabdi
50	64	32.0	481	1 6PGD_DROME	P41572 drosophila
51	64	32.0	481	1 6PGD_DROSI	P41573 drosophila
52	63	31.5	334	1 6PDA_CHLPN	Q92751 chlamydia p
53	62	31.0	330	1 6PDA_THETN	Q8r973 thermoaer
54	61	30.5	269	1 AROE_AQUAE	O67049 aquifex aeo
55	60	30.0	445	1 6PGD_CITAM	P41581 citrobacter
56	60	30.0	445	1 6PGD_CITDI	P41582 citrobacter
57	60	30.0	445	1 6PGD_ESCVU	P41574 escherichia
58	60	30.0	445	1 6PGD_KLEPL	P41575 klebsiella
59	60	30.0	445	1 6PGD_KLETE	P41577 klebsiella
60	60	30.0	473	1 6PGD_BUCAP	Q92hd9 buchnera ap
61	59	29.5	269	1 AROE_ARCFU	O27957 archaeoglob
62	59	29.5	294	1 MMSB_MYCTU	O53814 mycobacteri
63	59	29.5	445	1 6PGD_CITFR	P41583 citrobacter
64	59	29.5	445	1 6PGD_SHIBO	P41578 shigella bo
65	59	29.5	445	1 6PGD_SHIDY	P41579 shigella dy
66	59	29.5	445	1 6PGD_SHISO	P41580 shigella so
67	58.5	29.2	214	1 GLTI_YEAST	Q12680 saccharomyc
68	58	29.0	314	1 HCDH_HUMAN	Q16836 homo sapien
69	58	29.0	314	1 HCDH_MOUSE	Q61425 mus musculu
70	58	29.0	314	1 HCDH_PIG	P00348 sus scrofa
71	58	29.0	314	1 HCDH_RAT	Q9wvk7 rattus norv
72	58	29.0	334	1 6PDA_CHLCV	Q821m8 chlamydomphi
73	58	29.0	341	1 6PDA_XANAC	Q8pq9 xanthomonas
74	58	29.0	468	1 6PGD_BUCBP	Q89ax5 buchnera ap
75	57.5	28.7	444	1 HEMI_BACAA	Q811c5 bacillus an
76	57.5	28.7	456	1 GUDP_PSEPU	P42205 pseudomonas
77	57	28.5	117	1 Y12K_RHDV3	P27412 rabbit hemo
78	57	28.5	117	1 Y12K_RHDV3	P27413 rabbit hemo
79	57	28.5	334	1 6PDA_MYCBO	P59113 mycobacteri
80	57	28.5	340	1 6PDA_ENTFA	P59961 mycobacteri
81	57	28.5	468	1 6PGD_BUCAL	Q834c1 enterococcu
82	57	28.5	468	1 6PGD_BUCAL	P57208 buchnera ap
83	56.5	28.2	444	1 HEMI_BACCR	Q817q8 bacillus ce
84	56.5	28.2	446	1 HEMI_BACME	Q8gcb0 bacillus me
85	56.5	28.2	779	1 SRP_DROME	P52172 drosophila
86	56	28.0	332	1 6PDA_STAAM	Q99u16 staphylococ
87	56	28.0	332	1 6PDA_STAAM	Q89mw9 staphylococ
88	55	27.5	273	1 CME4_BACSU	P39696 bacillus su
89	55	27.5	296	1 PANE_VIBCH	Q9kpq9 vibrio chol
90	55	27.5	326	1 6PDA_BRAJA	Q89w0 bradyrhizob
91	55	27.5	334	1 6PDA_CHLMU	Q9pl12 chlamydia t
92	55	27.5	334	1 6PDA_CHLTR	O84719 chlamydia m
93	55	27.5	341	1 6PDA_PSESM	Q883y4 pseudomonas
94	55	27.5	341	1 6PDA_XANCP	Q893y4 xanthomonas
95	55	27.5	573	1 ERG1_RAT	P52020 rattus norv
96	54	27.0	223	1 TRKA_STRCO	Q53949 streptomyce
97	54	27.0	331	1 PYRB_PSVT1	Q934t0 psychrobact
98	54	27.0	339	1 GALE_NEIMA	P56997 neisseria m
99	54	27.0	339	1 GALE_NEIMB	P56985 neisseria m
100	54	27.0	339	1 GALE_NEIMC	P56986 neisseria m

ALIGNMENTS

RESULT 1

YKWC BACSU STANDARD; PRT; 288 AA.

ID YKWC BACSU STANDARD; PRT; 288 AA.

AC O34948;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical oxidoreductase ykwc (EC 1.1.1.-.-).

GN YKWC OR BSU13960.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC STRAIN=168;

RA Scanlan E., Devine K.M.;

RT "Sequence of the Bacillus subtilis chromosome from ykua to cse-15.";

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC MEDLINE=98044033; PubMed=9384377;

RA Kunz F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N., Guisepi G., Glaser P., Goffeau A., Gollightly E.J., Grandi G., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Koenigsstein G., Krogh S., Kumano M., Kobayashi Y., Koetter P., Koningstein G., Lauber J., Lazarevic V., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;

RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";

RL Nature 390:249-256(1997).

CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase family.

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CC EMBL; AJ222587; CAA10859.1; -.

DR EMBL; Z99111; CAB13269.1; -.

DR PIR; B69870; B69870.

DR Subtilist; BG13328; Ykwc.

DR InterPro; IPR002204; 3hydroxisobut_dh.

DR InterPro; IPR006183; 6PGD.

DR InterPro; IPR006115; 6PGD_NAD.

DR Pfam; PF03446; NAD_binding_2; 1.

DR PRINTS; PR00076; 6PGDHRGNASE.

DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.

KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.

FT ACT SITE 172 BY SIMILARITY.

SQ SEQUENCE 288 AA; 30711 MW; 976DD908DB47A30 CRC64;

Query Match 49.5%; Score 99; DB 1; Length 288;

Best Local Similarity 47.4%; Pred. No. 9.1e-06;

Matches 18; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFGLGLMGSGIVSNLLKMGHTVTVMNRATKCDLFIQ 38

DB 6 GFGLGVMGKSMASHILNDGHPVLVYTRYTKKAEISILQ 43

RESULT 2

6PGD_SYN7 STANDARD; PRT; 470 AA.

ID -6PGD_SYN7 STANDARD; PRT; 470 AA.

AC F21577;

DT 01-MAY-1991 (Rel. 18, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).

GN GND.

OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).

OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.

OX NCBI_TaxID=1140;

RN [1]

RP SEQUENCE FROM N.A., AND SUBSTRATE-BINDING SITE.

RC MEDLINE=90299831; PubMed=2113917;

RA Broedel S.E. Jr., Wolf R.E. Jr.;

RT "Genetic tagging, cloning, and DNA sequence of the Synecococcus sp. strain PCC 7942 gene (gnd) encoding 6-phosphogluconate dehydrogenase.";

RT J. Bacteriol. 172:4023-4031(1990).

RL [2]

RP SEQUENCE FROM N.A.

RA Culler D.C., Krogmann D.W.;

RL Submitted (APR-1991) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.

CC -!- PATHWAY: Hexose monophosphate shunt.

CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase family.

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CC EMBL; M55002; AAA27330.1; -.

DR EMBL; X58719; CAA11555.1; -.

DR PIR; S14628; S14628.

DR HSP; P00349; 2PGD.

DR InterPro; IPR008927; 6GDH_C-like.

DR InterPro; IPR006183; 6PGD.

DR InterPro; IPR006114; 6PGD_C.

DR InterPro; IPR006113; 6PGD-decarbox.

DR InterPro; IPR006115; 6PGD_NAD.

DR InterPro; IPR006184; 6PGD_BS.

DR Pfam; PF00393; 6PGD; 1.

DR Pfam; PF03446; NAD_binding_2; 1.

DR PRINTS; PR00076; 6PGDHRGNASE.

DR PROSITE; PS00461; 6PGD; 1.

DR Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.

KW EPIVR -> SRVVP (IN REF. 1).

FT CONFLICT 154 158 R -> A (IN REF. 1).

FT CONFLICT 407 407 AAERGIPVAFASLDYFDSYRSPA ->

FT CONFLICT 415 440 RQNEFRFRFCFGLRLQPARSLP (IN REF. 2).

FT DYFG -> TTC (IN REF. 1).

FT CONFLICT 449 452 ERTDRSGS -> KAPIALL (IN REF. 1).

FT CONFLICT 457 464


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FT CONFLICT 468 469 QW -> M (IN REF. 1).
SQ SEQUENCE 470 AA; 50860 MW; 72504ABD32594762 CRC64;

Query Match
Best Local Similarity 45.0%; Score 90; DB 1; Length 470;
Matches 16; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFI 37
Db 7 GLIGLAVNGENLALNIERNFSLTVYNTAKTBAFM 43

RESULT 3
6PGD CANAL STANDARD; PRT; 517 AA.
AC O1328;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN DOR14.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
ON NCBI_TaxID=5476;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1060;
RA Watanabe M., Ishii N., Arisawa M., Aoki Y.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC
CC EMBL; AB006102; BAA21690.1; -.
CC HSP; P00349; 2PGD.
CC InterPro; IPR008927; 6DGDH_C_like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006114; 6PGD_C.
CC InterPro; IPR006113; 6PGD_NAD.
CC InterPro; IPR006115; 6PGD_BS.
CC Pfam; PF00393; 6PGD; 1.
CC Pfam; PF03446; NAD binding 2; 1.
CC PRINTS; PR00076; 6PGDHRGNASE.
CC TIGRFAMs; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 517 AA; 56924 MW; 91E3F520PFCABF7A CRC64;

Query Match
Best Local Similarity 44.5%; Score 89; DB 1; Length 517;
Matches 15; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFIQ 38
Db 32 GLIGLAVNGENLALNIERNFSLTVYNTAKTBAFM 69

RESULT 4
6PGD STAAH STANDARD; PRT; 468 AA.
AC Q99TY2;

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DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND OR SAI342 OR MW1464.
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=158879, 196620;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Llan J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Vi Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kato C., Sekimizu K.,
RA Hiraoka H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiratsuka K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WM2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.I., Oguchi A.,
RA Nagai Y., Iwano M., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsuka K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC
CC EMBL; AF003134; BAB42604.1; -.
CC EMBL; AF004827; BAB95329.1; -.
CC PIR; G89930; G89930.
CC HSP; P00349; 2PGD.
CC SWISS-2DPAGE; Q99TY2; STAAH.
CC InterPro; IPR008927; 6DGDH_C_like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006184; 6PGD_BS.
CC InterPro; IPR006114; 6PGD_C.
CC InterPro; IPR006115; 6PGD_NAD.
CC Pfam; PF00393; 6PGD; 1.
CC Pfam; PF03446; NAD binding 2; 1.
CC PRINTS; PR00076; 6PGDHRGNASE.
CC TIGRFAMs; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
CC Complete proteome.
SQ SEQUENCE 468 AA; 51802 MW; 61A5C2CAF3CCD011 CRC64;

Query Match
Best Local Similarity 44.0%; Score 88; DB 1; Length 468;
Matches 15; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFIQ 38
Db 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFIQ 38

```

6 GVIGLAVMGKNLAWNIESRGYSVFNRSSEKXTDLWVE 43

Db

RESULT 5

D3HI DROME

ID D3HI DROME STANDARD; PRT; 324 AA.

AC Q9V8M5; Q9V8M6;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) (HIBADH).

DE CGL5093

GN Drosophila melanogaster (Fruit fly)

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=Berkley;

RC MEDLINE=20196006; PubMed=107311132;

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadiet E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K.J., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwa C., Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195 (2000).

RN [2]

RP REVISIONS, AND ALTERNATIVE SPLICING.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.B.;

RA "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review";

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).

RL

CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-methyl-3-oxopropanoate + NADH.

CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=Q9V8M5-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=Q9V8M5-2; Sequence=VSP_001281, VSP_001282;

CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase family.

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CC

EMBL; AB003798; AAF57638.2; --

DR EMBL; AB003798; AAF57638.2; --

DR FlyBase; FBgn0034390; CGI5093.

DR InterPro; IPR002204; 3hydroxisobut_dh.

DR InterPro; IPR006183; 6PGD.

DR InterPro; IPR006115; 6PGD_NAD.

DR Pfam; PF03446; NAD_binding_2; 1.

DR PRINTS; PR00076; 6PGDHDRGNASE.

DR PROSITE; PS00895; 3-HYDROXYISOBUT_DH; 1.

DR Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;

KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;

KW Transit peptide; Alternative splicing.

KW TRANSIT 1 25 MITOCHONDRION (BY SIMILARITY).

FT CHAIN 26 324 PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.

FT NP BIND 29 57 NAD (ADP PART) (POTENTIAL).

FT ACT SITE 196 196 BY SIMILARITY.

FT VARSPLIC 95 227 NADVASIDEMTADGVNKKDTIFIDSTISDPLVKSLQKITS AKGARFIDAVTSGVPGAEQATITFMVGTGEAYNAVYKAVL ECKGKITHGVYGMGAALKCNMMMLAISMGVSEAMNLLA VROGLDANVF -> KCRGPRVHQEDHDLRLHWGPGRQ AVQOHDAGHLDHDSGGSGGAPGSCQCLRDHQLHRT LLGLGLQPCARSLPQCSQGLRRFLGLSDHGGSGGLR SGQRFLQTHPAGISGAQGLFVAVR (in isoform Short).

FT /FTId=VSP_001281.

FT Missing (in isoform Short).

FT /FTId=VSP_001282.

FT VARSPLIC 228 324

FT SEQUENCE 324 AA; 33883 MW; A39B534753EAB83E CRC64;

Query Match 43.5%; Score 87; DB 1; Length 324;

Best Local Similarity 47.1%; Pred. No. 0.0004;

Matches 16; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OY 1 GFLGLGLMGSGIVSNLLKMGHTVTVTWNRATKCD 34

DB 32 GFVGLGNMGANWASNLKAGKHLHVFEDISKPAD 65

RESULT 6

6PGD STAAAM

ID 6PGD STAAAM STANDARD; PRT; 468 AA.

AC Q931R3;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).

GN GND OR SAV1511.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158878;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=21311952; PubMed=11418146;

RX

RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).

```
--!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC      5-phosphate + CO(2) + NADPH.
CC      -!- PATHWAY: Hexose monophosphate shunt.
CC      -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC          family.
-----
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CC or send an email to license@sib-sib.ch).
-----
DR       EMBL; AE002301; AAF39196.1; -.
DR       PIR; AB1714; AB1714.
DR       HSSP; P00349; 2PGD.
DR       TIGR; TC0333; -.
DR       InterPro; IPR008927; GGDH_C_like.
DR       InterPro; IPR006183; 6PGD_-.
DR       InterPro; IPR006114; 6PGD_C.
DR       InterPro; IPR006113; 6PGD_decarbox.
DR       InterPro; IPR006115; 6PGD_NAD.
DR       InterPro; IPR006184; 6PGDom_BS.
DR       Pfam; PF00393; 6PGD; 1.
DR       Pfam; PF03446; NAD_binding_2.
DR       PRINTS; PR00076; 6PGDHDRGNASE.
DR       TIGRFAMS; TIGR00873; gnd; 1.
DR       PROSITE; PS00461; 6PGD; 1.
KW Glucuronate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 479 AA; 52689 MW; 3501DD6DAAB0BFB CRC64;

Query Match              42.5%; Score 85; DR 1; Length 479;
Best Local Similarity    39.5%; Pred. No. 0.0011;
Matches   15; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Oy 1 GFGLGMLGGSGIVSNLLKMGHTVTVMNRTAEKCIDLFIQ 38
     |||:||||:||||:||||:||||:||||:||||:||||:
Db 7 GLIQLAVMKNLVNIIMIDHGFAVSVDYNSPEKTTEFLK 44

RESULT 8
6PGD CHLPN STANDARD; PERT; 479 AA.
ID _6PGD CHLPN QJ28I3; O9JC01.
AC AC
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating [EC 1.1.1.44].
GS ND OR CPN0360 OR CP0398 OR CPB0369.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=83558;
RN [1]
RP SEQUENCE FROM N.A.
RR STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RE Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
[2]
RP SEQUENCE FROM N.A.
RR STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., Deboy K., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
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RL Nucleic Acids Res. 28:1397-1406 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC 1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC 1- PATHWAY: Hexose monophosphate shunt.
CC 1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC
CC EMBL; AE001620; AAD18504.1; -
CC EMBL; AE002201; AAF38243.1; -
CC EMBL; AP002546; BAA98568.1; -
CC EMBL; AE017158; AAP98300.1; -
CC PIR; C72088; C72088.
CC PIR; F86535; F86535.
CC HSSP; P00349; 2PGD.
CC TIGR; CP0398; -
CC InterPro; IPR008927; 6GDGH_C_like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006114; 6PGD_C.
CC InterPro; IPR006113; 6PGD_decarbox.
CC InterPro; IPR006115; 6PGD_NAD.
CC Pfam; PF00393; 6PGD; 1.
CC Pfam; PF03446; NAD_binding_2; 1.
CC PRINTS; PR00076; 6PGDHDHGNASE.
CC TIGRPFAMs; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 479 AA; 52938 MW; 0FD301D3378E11FA CRC64;

Query Match 42.5%; Score 85; DB 1; Length 479;
Best Local Similarity 42.1%; Pred. No. 0.0011;
Matches 16; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVGNLLKMGHTVTVMNRTAEKCDLFIQ 38
DB 6 GLIGLAVGNKLVLLNMIDHGFVSQVYNRTPEKTRDFLK 43

RESULT 9
GARR_ECOLI STANDARD; PRT; 294 AA.
AC P23523;
AT 01-NOV-1991 (Rel. 20, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate
DE semialdehyde reductase) (TSAR).

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GN GARR OR B3125 OR C3880.
OS Escherichia coli, and
OS Escherichia coli O6
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91154140; PubMed=1705543;
RA Komine Y., Inokuchi H.;
RT "Precise mapping of the rnpB gene encoding the RNA component of RNase
RT P in Escherichia coli K-12.";
RL J. Bacteriol. 173:1813-1816 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9279503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=98447507; PubMed=9772162;
RA Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
RT "Evolution of enzymatic activities in the enolase superfamily:
RT characterization of the (D)-glucarate/galactarate catabolic pathway
RT in Escherichia coli.";
RL Biochemistry 37:14369-14375 (1998).
RN [5]
RP GENE NAME.
RX MEDLINE=20225875; PubMed=10762278;
RA Monterrubio R., Baldoni L., Obradors N., Aguilar J., Badia J.;
RA "A common regulator for the operons encoding the enzymes involved in
RA D-galactarate, D-glucarate, and D-glycerate utilization in
RA Escherichia coli.";
RL J. Bacteriol. 182:2672-2674 (2000).
CC 1- CATALYTIC ACTIVITY: (R)-glycerate + NAD(P)(+) = 2-hydroxy-3-
CC oxopropionate + NAD(P)H.
CC 1- PATHWAY: D-galactarate metabolism; third step.
CC 1- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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CC
CC EMBL; D90212; BAA14238.1; ALT_INIT.
CC EMBL; U18997; AAA57928.1; ALT_INIT.
CC EMBL; AE000394; AAC76159.1; ALT_INIT.
CC EMBL; AE016767; AAN82321.1; ALT_INIT.
CC EcoGene; EG11176; gar.
CC InterPro; IPR002204; 3hydroxisobut_dh.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006115; 6PGD_NAD.

```

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KW Guconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 488 AA; 52767 MW; FB69CCCA98DEE6B5 CRC64;

Query Match          42.0%; Score 84; DB 1; Length 488;
Best Local Similarity 43.2%; Pred. No. 0.0015;
Matches 16; Conservative 8; Mismatches 13; Indels 0; Gaps 0

QY      1 GFGLGMLMGSGIVSNLLKMGHTVTVMNRATAEKCDELFI 37
        |||::|||::|||::|||::|||::|||::|||::|||::
Db       6 FGIGLAVNGENLVNIERNRGSFVAVNRTTIVVDREL 42

RESULT 11
6PGD BACSU STANDARD; PRT; 468 AA.
AC PI2013;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GNTZ OR BSU40080.
OS Bacillus subtilis
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87008613; PubMed=3020045;
RA Fujita Y., Fujita T., Miwa Y., Nihashi J., Aratani Y.;
RT "Organization and transcription of the gluconate operon, of
RL Bacillus subtilis.";
RJ J. Biol. Chem. 261:13744-13753(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / BGSC1A1;
RA Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
RT "Cloning and sequencing of a 36-kb region of the Bacillus subtilis
RL genome between the gnt and iol operons.";
RJ DNA Res. 2:61-69(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuno V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Colglhtly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haelech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue J.C., Medigec C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogilwa K., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puig C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Toononi A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus

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RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
RT through comparison with genomes of *Escherichia coli* K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES= *S. flexneri*; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152; Venkatesan M.M., Deng W.,
RA Wei J., Goldberg M.B., Burland V., Plunkett G. III, Rose D.J., Darling A.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of *Shigella*
RT *flexneri* serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
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CC family.
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CC -----
DR EMBL; L19201; AAB03015.1; -;
DR EMBL; A8000464; AAD13444.1; -;
DR EMBL; A8015402; AAN45389.1; -;
DR EMBL; A8016990; AAP18811.1; -;
DR PIR; S40826; S40826.
DR EcoGene; EG11847; yihU.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD NAD.
DR Pfam; PF03446; NAD binding 2; 1.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
DR Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT ACT SITE 171 171 BY SIMILARITY.
SQ SEQUENCE 298 AA; 31158 MW; 74F8C809FA7881C CRC64;
Query Match 40.0%; Score 80; DB 1; Length 298;
Best Local Similarity 53.3%; Pred. No. 0.0031;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 2 FLGLGLMGSGIVSNLLKMGHTVTVNRTAE 31
Db 6 FLGLGQMGSPMASNLLKQGHQLRVFDVNAE 35
RESULT 14
YIHU SALTY STANDARD; PRT; 298 AA.
AC Q9L7S0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase yihU (EC 1.1.-.-).
GN yihU OR STW4023.
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Salmonella*.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Krogan N.J., Zhang R., Neuhard J., Kelln R.A.;
RT "Utilization of dihydroxotrate as sole pyrimidine source by *Salmonella*
RT *typhimurium*.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of *Salmonella enterica* serovar *Typhimurium*
RT LT2.";
RL Nature 413:852-856(2001).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC -----
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CC -----
DR EMBL; AF220438; AAP27921.1; -;
DR EMBL; A8008887; AAL22862.1; -;
DR StyGene; SG77777; yihU.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD NAD.
DR InterPro; IPR000205; NAD-ES.
DR Pfam; PF03446; NAD binding 2; 1.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
DR Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT ACT SITE 171 171 BY SIMILARITY.
SQ SEQUENCE 298 AA; 31280 MW; 7ED9FA174249240C CRC64;
Query Match 40.0%; Score 80; DB 1; Length 298;
Best Local Similarity 57.7%; Pred. No. 0.0031;
Matches 15; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 FLGLGLMGSGIVSNLLKMGHTVTVN 27
Db 6 FLGLGQMGSPMASNLLKQGHQLSVFD 31
RESULT 15
6PGD TRYBB STANDARD; PRT; 479 AA.
ID 6PGD TRYBB
AC F31072;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND.
OS *Trypanosoma brucei brucei*.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RX MEDLINE=93149212; PubMed=8426618;
RA Barrett M.P., le Page R.W.F.;
RT "A 6-phosphogluconate dehydrogenase gene from *Trypanosoma brucei*.";
RL Mol. Biochem. Parasitol. 57:89-100(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=98411456; PubMed=9737929;
RA Phillips C., Dohnalek J., Gover S., Barrett M.P., Adams M.J.;
RT "A 2.8-A resolution structure of 6-phosphogluconate dehydrogenase
RT from the protozoan parasite *Trypanosoma brucei*: comparison with the
RT sheep enzyme accounts for differences in activity with coenzyme and
RT substrate analogues.";
RL J. Mol. Biol. 282:667-681(1998).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.

CC -!- PATHWAY: Hexose monophosphate shunt.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase family.
 CC
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CC EMBL: X65623; CAA46577.1; --
 CC PIR: A48565; A48565
 CC PDB: 1PGJ; 11-NOV-98.
 CC InterPro: IPR008927; 6DGDH_C-like.
 CC InterPro: IPR006183; 6PGD.
 CC InterPro: IPR006114; 6PGD_C.
 CC InterPro: IPR006113; 6PGD decarbox.
 CC InterPro: IPR006115; 6PGD_NAD.
 CC InterPro: IPR006184; 6PGDm_BS.
 CC Pfam: PF00393; 6PGD; 1.
 CC Pfam: PF03446; NAD-binding 2; 1.
 CC PRINTS: PR00076; 6PGDHDRGNASE.
 CC TIGRFAMs: TIGR00873; gnd; 1.
 CC PROSITE: PS00461; 6PGD; 1.
 CC Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
 KW 3D-structure.

KW 3D-structure. 3 3
 FT STRAND 3 3
 FT STRAND 5 8
 FT HELIX 12 23
 FT TURN 24 25
 FT STRAND 28 31
 FT HELIX 35 44
 FT TURN 45 47
 FT TURN 49 50
 FT HELIX 51 53
 FT STRAND 54 56
 FT HELIX 60 66
 FT STRAND 67 67
 FT STRAND 72 75
 FT HELIX 81 93
 FT TURN 96 97
 FT STRAND 99 102
 FT HELIX 108 119
 FT TURN 120 122
 FT STRAND 124 131
 FT HELIX 133 139
 FT STRAND 142 147
 FT HELIX 149 162
 FT STRAND 165 165
 FT TURN 167 168
 FT STRAND 171 171
 FT TURN 179 180
 FT HELIX 181 209
 FT TURN 210 211
 FT HELIX 214 226
 FT TURN 227 227
 FT STRAND 229 230
 FT STRAND 232 232
 FT HELIX 233 243
 FT STRAND 245 245
 FT TURN 247 248
 FT STRAND 251 251
 FT HELIX 252 255
 FT STRAND 256 256
 FT HELIX 265 276
 FT TURN 277 277
 FT HELIX 281 294
 FT TURN 295 295
 FT HELIX 296 305
 FT TURN 307 310

FT TURN 322 323
 FT HELIX 325 356
 FT HELIX 362 367
 FT TURN 368 369
 FT TURN 374 375
 FT STRAND 377 377
 FT TURN 378 379
 FT HELIX 380 389
 FT TURN 391 392
 FT TURN 396 397
 FT HELIX 398 400
 FT HELIX 401 421
 FT HELIX 427 439
 FT TURN 440 440
 FT TURN 445 445
 FT HELIX 446 458
 FT STRAND 462 464
 FT STRAND 470 471
 SQ SEQUENCE 479 AA; 52153 MW; 64FED260915ABC2F CRC64;
 Query Match 40.0%; Score 80; DB 1; Length 479;
 Best Local Similarity 39.5%; Pred. No. 0.0049;
 Matches 15; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 GFLGLMGSGIVSNLLKMGHTVTVMRTAEKCDLFIQ 38
 Db 6 GVGLGVGAGNALNIAEKGVAVFNRTYSKSEFMK 43

RESULT 16
 6PGD HAEIN
 ID 6PGD HAEIN STANDARD; PRT; 484 AA.
 AC P43774;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
 GN GND OR HI0553.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OC NCBI_TaxID=727;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Rd / KW20 / ATCC 51907;
 RC MEDLINE=95350630; PubMed=7542800;
 RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Haudok D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
 CC 5-phosphate + CO(2) + NADPH.
 CC -!- PATHWAY: Hexose monophosphate shunt.
 CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase family.
 CC
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 CC -----
 CC EMBL: U32737; AAC22210.1; --
 DR


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DR PIR; C64077; C64077.
DR HSSP; P00349; 2PGD.
DR TIGR; H10553; -.
DR InterPro; IPR008927; 6GDH_C_like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD C.
DR InterPro; IPR006113; 6PGD decarbox.
DR InterPro; IPR006115; 6PGD NAD.
DR Pfam; PF00393; 6PGD; 1.
DR PRINTS; PR00076; NAD binding 2; 1.
DR InterPro; IPR006184; 6PGDm_BS.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
DR TIGRFAMS; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 484 AA; 53140 MW; 8381EEB3C704C5DA CRC64;

Query Match 40.0%; Score 80; DB 1; Length 484;
Best Local Similarity 39.5%; Pred. No. 0.0049;
Matches 15; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38
DB 8 GVIGLAVMGQNLILNMNDHGFVKVAYNRTTSKVDFLQ 45

RESULT 17
6PG2_YEAST
ID 6PG2_YEAST STANDARD; PRT; 492 AA.
AC P53319;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating 2 (EC 1.1.1.44).
GN GND2 OR YGR256W OR G9170.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97279233; PubMed=9133741;
RA Mazzoni C., Ruzzi M., Rinaldi T., Solinas F., Montebove F.,
RA Frontali L.;
RT "Sequence analysis of a 10.5 kb DNA fragment from the yeast
RT chromosome VII reveals the presence of three new open reading frames
RT and of a tRNAThr gene.";
RL Yeast 13:369-372(1997).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC
CC -----
CC EMBL; X99228; CAA67612.1; -.
CC DR EMBL; Z73041; CAA97285.1; -.
CC PIR; S64588; S64588.
CC DR HSSP; P00349; 2PGD.
CC GERMOnline; 141568; -.
CC DR SGD; S0003488; GND2.
CC DR GO; GO:0004616; F:6-phosphogluconate dehydrogenase (decarboxyla. .; IMP.
CC DR GO; GO:0006006; P:glucose metabolism; IGI.
CC InterPro; IPR008927; 6GDH_C_like.

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DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD C.
DR InterPro; IPR006113; 6PGD decarbox.
DR InterPro; IPR006115; 6PGD NAD.
DR Pfam; PF00393; 6PGD; 1.
DR PRINTS; PR00076; NAD binding 2; 1.
DR TIGRFAMS; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 492 AA; 53922 MW; 3D75D53563987735 CRC64;

Query Match 40.0%; Score 80; DB 1; Length 492;
Best Local Similarity 40.5%; Pred. No. 0.005;
Matches 15; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFI 37
DB 9 GLVGLAVMGQNLILNADHGFVTVAYNRTQSKVDRL 45

RESULT 18
6PG2_BACSU
ID 6PG2_BACSU STANDARD; PRT; 468 AA.
AC P80859; P54546;
DT 01-OCT-1996 (Rel. 34, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating II (EC 1.1.1.44)
DE (GNT211).
GN YQJ1 OR BSU23860.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes.";
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Barbero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solido B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

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SEQUENCE FROM N.A.
RA Desouza M., Lobo Z., Maitra P.K.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaaski E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
Vaadin M.;
RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
VIII";
RN Science 265:2077-2082 (1994).
[3]
RP SEQUENCE OF 41-47 AND 120-131.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a *Saccharomyces cerevisiae* protein
database";
RL Electrophoresis 15:1466-1486 (1994).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.

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DR EMBL; Z46631; CAA86600.1; -;
DR EMBL; U00028; AAB68452.1; -;
DR EMBL; U17155; AAA33637.1; -;
DR PIR; S46671; S46671.
DR HSSP; P00349; 2PGD.
DR GerMOnline; 139501; -;
DR SGD; S0001226; GND1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IMP.
DR GO; GO:0060006; P:glucose metabolism; IGI.
DR InterPro; IPR008927; 6DGDH_C_like.
DR InterPro; IPR006113; 6PGD_C.
DR InterPro; IPR006114; 6PGD_Gecarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR TIGRFAMs; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
DR Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
DR Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 489 AA; 53543 MW; 55CAE5DACDC6A00B CRC64;

Query Match 39.5%; Score 79; DB 1; Length 489;
Best Local Similarity 40.5%; Pred. No. 0.0067;
Matches 15; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRRTAEKCDLFI 37
DB 6 GLIGLAVMGQNLILNAADHGFTVCAYNRTQSKVDHFL 42

RESULT 21
6PGD ACTAC
ID -6PGD ACTAC STANDARD; PRT; 484 AA.
AC P70718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND.
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Y4;
RX MEDLINE=97148607; PubMed=9020051;
RA Yoshida Y., Nakano Y., Yamashita Y., Koga T.;
RT "The gnd gene encoding a novel 6-phosphogluconate dehydrogenase and
RT its adjacent region of *Actinobacillus actinomycetemcomitans*
RT chromosomal DNA";
RL Biochem. Biophys. Res. Commun. 230:220-225 (1997).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.

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DR EMBL; D88189; BAA13558.1; -;
DR PIR; JCS282; JCS282.
DR HSSP; P00349; 2PGD.
DR InterPro; IPR008927; 6DGDH_C_like.
DR InterPro; IPR006113; 6PGD_C.
DR InterPro; IPR006114; 6PGD_Gecarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR006118; 6PGD_BS.
DR Pfam; PF03446; NAD binding 2; 1.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR TIGRFAMs; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
DR Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
DR Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 484 AA; 53288 MW; F7BD0B2EA3BF624D CRC64;

Query Match 38.5%; Score 77; DB 1; Length 484;
Best Local Similarity 36.8%; Pred. No. 0.012;
Matches 14; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRRTAEKCDLFIQ 38
DB 8 GVIGLAVMGQNLILNNDHGFKVAVNRTTSKVDFLE 45

RESULT 22
MMSB PSEAE
ID MMSB PSEAE STANDARD; PRT; 298 AA.
AC P28811;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH).
GN MMSB OR PA3569.
OS Pseudomonas aeruginosa.

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RA opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
CC methyl-3-oxopropanoate + NADH.
CC -!- PATHWAY: Distal valine metabolic pathway.
CC -!- INDUCTION: By valine.
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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CC
CC -----
DR EMBL; M84911; AAA25892.1; -.
DR EMBL; AE004778; AAG06957.1; -.
DR PIR; C42902; C42902.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6FGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
KW Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 3 31 NAD (BY SIMILARITY).
FT ACT_SITE 171 171 BY SIMILARITY.
SQ SEQUENCE 298 AA; 30486 MW; 0C4D7B5A7C870730 CRC64;

Query Match 37.5%; Score 75; DB 1; Length 298;
Best Local Similarity 57.7%; Pred. NO. 0.014;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 FLGLMGSGIVSNLLKMGHTVTYWN 27
Db 6 FLGLGNMGPGPMAANLLKAGHRVNVFD 31

RESULT 23
D3H1 ARATH
ID D3H1 ARATH STANDARD; PRT; 347 AA.
AC Q9SUC0; Q8LC25;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
DE (EC 1.1.1.31) (HIBADB).
GN AT4G20930 OR T13K14.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Bacteria; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Mueller M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Schmidheini T.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Moutry M., Bancroft I.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weljens I., Voet M., Bastiaens I., Aert R., Braum E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Molijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Faravanti E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdr F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RT Nature 402:769-777(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
CC methyl-3-oxopropanoate + NADH.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC -!- CAUTION: Ref.1 sequences differ from that shown due to erroneous
CC gene model prediction.
CC
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CC -----
CC EMBL; AL080282; CAB45888.1; ALT_SEQ.
CC EMBL; AL161554; CAB75093.1; ALT_SEQ.
CC EMBL; AY086845; AAM63893.1; -.
CC InterPro; IPR002204; 3hydroxisobut dh.
CC PROSITE; PS00895; 3-HYDROXYISOBUT DH; 1.
CC Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 34 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 35 347 PROBABLE 3-HYDROXYISOBUTYRATE
FT NP_BIND 38 66 NAD (ADP PART) (POTENTIAL).
FT ACT_SITE 219 219 BY SIMILARITY.
FT CONFLICT 21 21 S -> F (IN REF. 2).
SQ SEQUENCE 347 AA; 37364 MW; 6ED2E87CC3DE191C CRC64;

Query Match 37.5%; Score 75; DB 1; Length 347;
Best Local Similarity 39.5%; Pred. No. 0.016;
Matches 15; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFIQ 38
DB 41 GFILGNMGFRWNNLIRAGYKVTVDINRDVNMKMFTE 78

RESULT 24
6PGD_STAEP STANDARD; PRT; 468 AA.
AC Q8CF47;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND OR SELL192.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]_TaxID=1282;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Qiu Z.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qiu Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y.-Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593 (2003).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC -----
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CC -----
CC EMBL; AE016748; AAO04791.1; -.
CC InterPro; IPR008927; 6GDH_C like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006184; 6PGDm_BS.
CC InterPro; IPR006114; 6PGD C.
CC InterPro; IPR006113; 6PGD decarbox.
CC InterPro; IPR006115; 6PGD_NAD.
CC Pfam; PF00393; 6PGD; 1.
CC Pfam; PF03446; NAD binding 2; 1.
CC PRINTS; PR00076; 6PGDHDRGNASE.
CC TIGRFAMs; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 468 AA; 53102 MW; F756DDFF3D21EFB2 CRC64;

Query Match 37.5%; Score 75; DB 1; Length 485;
Best Local Similarity 37.8%; Pred. No. 0.023;
Matches 14; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFI 37
DB 9 GLIGLAVMGQNLILNNDHGFVVCAYNRTTSKVDDFL 45
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DR PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
SQ SEQUENCE 468 AA; 52234 MW; A4738F224237494E CRC64;

Query Match 37.5%; Score 75; DB 1; Length 468;
Best Local Similarity 34.2%; Pred. No. 0.022;
Matches 13; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFIQ 38
DB 6 GYVGLAVMGKLNLAWNIEGRGYSVYNRSRQKTDEWVK 43

RESULT 25
6PGD_CUNEL STANDARD; PRT; 485 AA.
AC Q60037;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN 6-PGD.
OS Cunninghamella elegans.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Cunninghamellaceae; Cunninghamella.
OX NCBI_TaxID=4853;
RN [1]_TaxID=4853;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 36112;
RX MEDLINE=99085678; PubMed=9868787;
RA Wang R.F., Khan A.A., Cao W.W., Cerniglia C.E.;
RT "Identification and sequencing of a cDNA encoding 6-phosphogluconate
RT dehydrogenase from a fungus, Cunninghamella elegans and expression of
RT the gene in Escherichia coli.";
RL FEMS Microbiol. Lett. 169:397-402 (1998).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC -----
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CC -----
CC EMBL; Y17297; CAA76734.1; -.
CC KSSP; P00349; 2PGD.
CC InterPro; IPR008927; 6GDH_C like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006114; 6PGD C.
CC InterPro; IPR006113; 6PGD decarbox.
CC InterPro; IPR006115; 6PGD_NAD.
CC InterPro; IPR006184; 6PGDm_BS.
CC Pfam; PF00393; 6PGD; 1.
CC Pfam; PF03446; NAD binding 2; 1.
CC PRINTS; PR00076; 6PGDHDRGNASE.
CC TIGRFAMs; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 485 AA; 53102 MW; F756DDFF3D21EFB2 CRC64;

Query Match 37.5%; Score 75; DB 1; Length 485;
Best Local Similarity 37.8%; Pred. No. 0.023;
Matches 14; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFI 37
DB 9 GLIGLAVMGQNLILNNDHGFVVCAYNRTTSKVDDFL 45
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[illegible][illegible]

28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND OR STM2081.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=89364685; PubMed=2671649;
RA Reeves P., Stevenson G.;
RT "Cloning and nucleotide sequence of the Salmonella typhimurium LT2
gnd gene and its homology with the corresponding sequence of
Escherichia coli K12.";
RL Mol. Gen. Genet. 217:182-184 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX Dykhuizen D.E., Green L.;
RA Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanders K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856 (2001).
RN [4]
RP SEQUENCE OF 1-57 FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=91260454; PubMed=1710759;
RA Jiang X.M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
RT "Structure and sequence of the rfb (O antigen) gene cluster of
RT Salmonella serovar typhimurium (strain LT2).";
RL Mol. Microbiol. 5:695-713 (1991).
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -1- PATHWAY: Hexose monophosphate shunt.
CC -1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC -----
CC EMBL; X15651; CAA33677.1; -.
CC EMBL; M64332; AAA27137.1; -.
CC EMBL; AE008792; AAL20985.1; -.
CC EMBL; X56793; CAA40131.1; -.
CC F1R; S04397; S04397.
CC HSP; P00349; 2PGD.
CC InterPro; IG0146; gnd.
CC InterPro; IPR008927; 6GDH_C_like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR06114; 6PGD_C.
CC InterPro; IPR06113; 6PGD decarbox.
CC InterPro; IPR06115; 6PGD NAD.
CC InterPro; IPR006184; 6PGDm_BS.
CC Pfam; PF00393; 6PGD; 1.
CC PRINTS; PR00076; NAD_binding_2; 1.
CC TIGRfams; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
CC

KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 468 AA; 51395 MW; D8EB53A2DAADB7 CRC64;
Query Match 37.0%; Score 74; DB 1; Length 468;
Best Local Similarity 38.2%; Pred. No. 0.03;
Matches 13; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRTEAKCD 34
Db 7 GVVGMAVGNRLALNIESRGYTVSVNRSREKTE 40
RESULT 29
6PGD_CERCA STANDARD; PRT; 481 AA.
ID -6PGD_CERCA
AC P41570;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN PGD.
OS Ceratitidis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitidis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94093871; PubMed=8269100;
RA Scott M.J., Kriticou D., Robinson A.S.;
RT "Isolation of cDNAs encoding 6-phosphogluconate dehydrogenase and
RT glucose-6-phosphate dehydrogenase from the Mediterranean fruit fly
RT Ceratitidis capitata: correlating genetic and physical maps of
RT chromosome 5.";
RL Insect Mol. Biol. 1:213-222 (1993).
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -1- PATHWAY: Hexose monophosphate shunt.
CC -1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC -----
CC EMBL; S67873; AAB29396.1; -.
CC HSP; P00349; 2PGD.
CC InterPro; IPR008927; 6GDH_C_like.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR06114; 6PGD_C.
CC InterPro; IPR006113; 6PGD decarbox.
CC InterPro; IPR006115; 6PGD NAD.
CC InterPro; IPR006184; 6PGDm_BS.
CC Pfam; PF00393; 6PGD; 1.
CC PRINTS; PR00076; NAD_binding_2; 1.
CC TIGRfams; TIGR00873; gnd; 1.
CC PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
SQ SEQUENCE 481 AA; 52963 MW; F0ABB506AD1B86D0 CRC64;
Query Match 37.0%; Score 74; DB 1; Length 481;
Best Local Similarity 38.9%; Pred. No. 0.03;
Matches 14; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
QY 3 LGFLMGSGIVSNLLKMGHTVTWNRTEAKCDLFQ 38
Db 10 IGLAVMGQNLVLMNDKGFVVCAYNFTVEKVNQFLK 45

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DR  InterPro; IPR008927; 6DGDH_C-like.
DR  InterPro; IPR006183; 6PGD.
DR  InterPro; IPR006114; 6PGD C.
DR  InterPro; IPR006113; 6PGD decarbox.
DR  InterPro; IPR006115; 6PGD NAD.
DR  InterPro; IPR006184; 6PGdom_BS.
DR  Pfam; PF00393; 6PGD; 1.
DR  Pfam; PF03446; NAD_binding_2; 1.
DR  PRINTS; PR00076; 6PGDHDHGNASE.
DR  TIGRFAMs; TIGR00873; gnd; 1.
DR  PROSITE; PS00461; 6PGD; 1.
DR  KW Oxidoreductase; Pentose shunt; NADP.
FT  CONFLICT 219 220      IA -> ST (IN REF. 1).
SQ  SEQUENCE 492 AA; 53679 MW; F55F342957A9D3E1 CRC64;

Query Match          37.0%; Score 74; DB 1; Length 492;
Best Local Similarity 37.8%; Pred. No. 0.031;
Matches 14; Conservative 7; Mismatches 16; Indels

Qy  1  GFLGLGMGSGIVSNLLKMGHTVTWVNTTAERKDLFI 37
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  10  GLIGLAVMGQNILNGADKGFVCCYNITTSVDEFL 46

Search completed: September 16, 2004, 07:46:09
Job time : 12 secs

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Search completed: September 16, 2004, 07:46:09
Job time : 12 secs

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RESULT 30
6PGD SCHPO STANDARD; PRT; 492 AA.
ID 6PGD SCHPO STANDARD; PRT; 492 AA.
DT P78812; Q9UOW5;
AC 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN SPBC660.16.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=PR745;
RC STRAIN=981162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RL DNAS.";
RL DNA Res. 4:363-369 (1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC STRAIN=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth I., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Laureau V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dega R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovskii G.V., Ussery D., Barrall B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC -1- 5-phosphate + CO(2) + NADPH.
CC -1- PATHWAY: Hexose monophosphate shunt.
CC -1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial/
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@sb-sib.ch).
CC
DR EMBL; D89161; BAA13823.1; ALT_INIT.
DR EMBL; AL034563; CAA22536.1; -.
DR FIC; T40628; T40628.
DR HSSP; P00349; 2PGD.
DR GeneDB Spombe; SPBC660.16; -.

```


Q8VIV7 mycobacteri
P95165 mycobacteri
Q94KU2 spinacia ol
Q92PA2 rhizobium m
Q8FBG0 escherichia
Q8VAX7 brucella me
Q8FXG6 brucella su
Q92PE1 rhizobium m
Q9CKG2 pasteurella
Q7VMX4 haemophilus
Q876H9 saccharomyc

ALIGNMENTS

RESULT 1

Q9BT11 Q9BT11 PRELIMINARY; PRT; 523 AA.
AC Q9BT11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN cDNA 3930401K13 gene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003693; AA03693.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; E:DNA binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000313; PWWP_domain.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00384; AT hook; 1.
DR PROSITE; PS0812; PWWP; 1.
FT NON_TER 1
SQ SEQUENCE 523 AA; 57215 MW; ED3E2853938A211F CRC64;

Query Match 100.0%; Score 200; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Non_Ter 1

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38
DB 241 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 278
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RESULT 2
Q922P9 Q922P9 PRELIMINARY; PRT; 546 AA.
AC Q922P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 3930401K13 gene.
GN NPAC OR 3930401K13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003693; AA03693.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; E:DNA binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000313; PWWP_domain.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF03446; NAD_binding_2; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00384; AT hook; 1.
DR PROSITE; PS0812; PWWP; 1.
FT NON_TER 1
SQ SEQUENCE 523 AA; 57215 MW; ED3E2853938A211F CRC64;

Query Match 100.0%; Score 200; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Non_Ter 1

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38
DB 241 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 278
|||||
RESULT 2
Q922P9 Q922P9 PRELIMINARY; PRT; 546 AA.
AC Q922P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 3930401K13 gene.
GN NPAC OR 3930401K13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003693; AA03693.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; E:DNA binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000313; PWWP_domain.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF03446; NAD_binding_2; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00384; AT hook; 1.
DR PROSITE; PS0812; PWWP; 1.
FT NON_TER 1
SQ SEQUENCE 523 AA; 57215 MW; ED3E2853938A211F CRC64;

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006893; AA06893.1; -.
DR MGD; MGI:1921272; Npac.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000313; PWWP_domain.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF03446; NAD_binding_2; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00384; AT hook; 1.
DR PROSITE; PS0812; PWWP; 1.
SQ SEQUENCE 546 AA; 59715 MW; F5D2090DE1F64723 CRC64;

Query Match 83.0%; Score 166; DB 11; Length 546;
Best Local Similarity 100.0%; Pred. No. 4.3e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Non_Ter 1

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
DB 270 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 301
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RESULT 3
Q9CYQ1 Q9CYQ1 PRELIMINARY; PRT; 546 AA.
AC Q9CYQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3930401K13RIK protein.
GN NPAC OR 3930401K13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK014456; BAB29363.1; -.
DR MGD; MGI:1921272; Npac.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR000313; PWWP_domain.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF03446; NAD_binding_2; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00384; AT hook; 1.
DR PROSITE; PS0812; PWWP; 1.
FT NON_TER 1
SQ SEQUENCE 546 AA; 59715 MW; F5D2090DE1F64723 CRC64;

DR InterPro: IPR006115; GPGD NAD.
 DR InterPro: IPR000637; AT hook.
 DR InterPro: IPR000313; PWWP_domain.
 DR Pfam: PF021178; AT_hook; 1.
 DR Pfam: PF03446; NAD_binding_2; 1.
 DR Pfam: PF00855; PWWP; 1.
 DR SMART: SM00384; AT_hook; 1.
 DR PROSITE: PS0812; PWWP; 1.
 SQ SEQUENCE 546 AA; 59744 MW; B3AC1562477ABCF CRC64;

Query Match 83.0%; Score 166; DB 11; Length 546;
 Best Local Similarity 100.0%; Pred. No. 4.3e-13;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTEAK 32
 DB 270 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTEAK 301
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RESULT 4
 Q9BXK2 PRELIMINARY; PRT; 547 AA.
 AC Q9BXK2; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome-like nuclear factor n-pac.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA New L., Han J.;
 RT "A novel cytokine-like nuclear factor, n-pac";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RM EMBL: AF215966; AAK15524.1; -;
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0004616; F:phosphoglucanase dehydrogenase (decarboxyla. . .); IEA.
 DR GO: GO:0006098; P:ribose-phosphate shunt; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR006115; GPGD NAD.
 DR InterPro: IPR000637; AT hook.
 DR InterPro: IPR000313; PWWP_domain.
 DR Pfam: PF021178; AT_hook; 1.
 DR Pfam: PF03446; NAD_binding_2; 1.
 DR Pfam: PF00855; PWWP; 1.
 DR SMART: SM00384; AT_hook; 1.
 DR PROSITE: PS0812; PWWP; 1.
 SQ SEQUENCE 547 AA; 59827 MW; C7D785CCBF83204A CRC64;

Query Match 83.0%; Score 166; DB 4; Length 547;
 Best Local Similarity 100.0%; Pred. No. 4.3e-13;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTEAK 32
 DB 271 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTEAK 302
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RESULT 5
 Q8T079 PRELIMINARY; PRT; 602 AA.
 AC Q8T079; Q9VL51;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE LD22344D (CG4747-PA).
 GN BEST:LD22483 OR BEST:LD29743 OR CG4747.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Burtis K.C., Busam D.A., Butler H., Brokstein P., Brottier P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler K., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradscky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
 RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
 RA Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 EMBL: AY069497; AAL39642.1; -.

DR	EWBL; AE003627; AAF52846.3; ...
DR	FlyBase; FBgn0043456; BEST:ID22483.
DR	GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla...); IEA.
DR	GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR	InterPro; IPR006115; 6PGD_NAD.
DR	InterPro; IPR000313; PWMP_domain.
DR	Pfam; PF03446; NAD_binding_2; 1.
DR	Pfam; PF00855; PWMP; 1.
DR	SMART; SM00293; PWMP; 1.
DR	PROSITE; PSS0812; PWMP; 1.
SQ	SEQUENCE 602 AA; 65252 MW; B004EEC610C23625 CRC64;
Query Match 63.0%; Score 126; DB 5; Length 602;	
Best Local Similarity 60.5%; Pred.No. 7.4e-08;	
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;	
QY	1 GFLGLGIMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38 :: :: : :: :
Dd	319 GFLGLGMGSITVKDLIYTGHKVVWNRITDKQPPAE 356 :: :: : :: :
RESULT 6	
ID Q94A74	PRELIMINARY; PRT; 248 AA.
AC Q94A74;	
DT 01-DEC-2001	(TrEMBLrel. 19, Created)
DT 01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DE AT3G25530/MWL2.15.	
OS Arabidopsis thaliana (Mouse-ear cress).	
OC Eukaryota; Viridiplantae; Streptophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eucots; rosids;	
OC eurosids II; Brassicales; Brassicaceae; Arabidopsais.	
OX NCBI_TaxID=3702;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,	
RA Bowser L., Carncini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,	
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.	
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,	
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.B., Sakurai T.,	
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,	
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,	
RA Ecker J.R.;	
RL "Arabidopsis cdna clones";	
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	
DR EWBL; AY049298; AAK83640.1; -	
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.	
DR GO; GO:0004616; F:phosphoglucuronate dehydrogenase (decarboxyla...); IEA.	
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.	
DR GO; GO:0006573; P:valine metabolism; IEA.	
DR InterPro; IPR002204; 3hydroxisobut_dh.	
DR InterPro; IPR006183; 6PGD	
DR InterPro; IPR006115; 6PGD_NAD.	
DR Pfam; PF03446; NAD_binding_2; 1.	
DR PRINTS; PR00076; 6PGDHDRGNASE.	
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.	
SQ SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;	
Query Match 62.5%; Score 125; DB 10; Length 248;	
Best Local Similarity 60.5%; Pred.No. 3.9e-08;	
Matches 23; Conservative 4; Mismatches 11; Indels 0; Gaps 0;	
QY	1 GFLGLGIMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38 :: :: : :: :
Dd	4 GFLGLGIMGKAMSNLLKNGFKVTVNRTLSKCDELVE 41 :: :: : :: :
RESULT 7	
ID Q94B07	PRELIMINARY; PRT; 289 AA.
AC Q94B07;	
DT 01-DEC-2001	(TrEMBLrel. 19, Created)

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DR InterPro; IPR006115; 6PGD NAD.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
SQ SEQUENCE 289 AA; 30691 MW; 3567002A19706636 CRC64;

Query Match 62.5%; Score 125; DB 10; Length 289;
Best Local Similarity 60.5%; Pred. No. 4.5e-08;
Matches 23; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFIQ 38
Dd 4 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCDLFIQ 41

RESULT 9
ID Q8LQJ7 PRELIMINARY; PRT; 343 AA.
AC Q8LQJ7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Atg17650).
GN Atg17650.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfosky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RA "Full-length messenger RNA sequences greatly improve genome
RA annotation.";
RA Genome Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Heuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA "Arabidopsis ORF clones.";
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP EMBL; AY093135; AAM13134.1; -.
DR EMBL; AY085690; AAM62909.1; -.
DR EMBL; BT008734; AAP42747.1; -.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR006115; 6PGD NAD.
DR Pfam; PF03446; NAD binding_2; 1.
DR Hypothetical protein.
SQ SEQUENCE 343 AA; 36287 MW; D012C16284C5FAS2 CRC64;

Query Match 61.5%; Score 123; DB 10; Length 343;
Best Local Similarity 64.7%; Pred. No. 9.9e-08;
Matches 23; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCD 34
Dd 4 GFLGLGMLGSGIVSNLLKMGHTVTVWNRATKCD 41

RESULT 9
ID Q8LQJ7 PRELIMINARY; PRT; 343 AA.
AC Q8LQJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Putative gamma hydroxybutyrate dehydrogenase.
GN B1151A10.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
   clone:B1151A10.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003413; BAB91904.1; -.
DR Gramene; Q8LQJ7; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PROSITE; PS00895; 3-HYDROXYISOBUT_DH; 1.
SQ SEQUENCE 343 AA; 35481 MW; 195ABBEDA048F84D CRC64;

Query Match 60.5%; Score 121; DB 10; Length 343;
Best Local Similarity 64.7%; Pred. No. 1.8e-07;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCD 34
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 54 GFLGLGINGAFMASNLINAGCDVTVMNRTSKCD 87

RESULT 12
Q84VC8 PRELIMINARY; PRT; 293 AA.
ID Q84VC8;
AC Q84VC8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 25, Last annotation update)
DE Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical
   protein).
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C.,
   Goff S., Glazebrook J.;
RT "Identification of Rice (Oryza sativa) Proteins Linked to the Cyclin-
   Mediated Regulation of the Cell Cycle.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RC TiSSUE=Panicle;
RA Moriguchi K., Ito Y., Yamazaki Y., Kurata N.;
RT "Finding of various plant nuclear proteins using yeast nuclear
   transportation trap system - a proteomal approach.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY224558; RAO72678.1; -.
DR EMBL; AB110167; BAC7859.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR006183; 6PGD_NAD.

DE Putative gamma hydroxybutyrate dehydrogenase.
GN B1151A10.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
   clone:B1151A10.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003413; BAB91904.1; -.
DR Gramene; Q8LQJ7; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PROSITE; PS00895; 3-HYDROXYISOBUT_DH; 1.
SQ SEQUENCE 343 AA; 35481 MW; 195ABBEDA048F84D CRC64;

Query Match 59.0%; Score 118; DB 10; Length 293;
Best Local Similarity 63.6%; Pred. No. 3.7e-07;
Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 33
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 4 GFLGLGIMGKAMAANLLRHGRVTVVNRTLK 36

RESULT 13
Q97DX8 PRELIMINARY; PRT; 292 AA.
ID Q97DX8;
AC Q97DX8;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 24, Last annotation update)
DE Dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC
   B.subtilis ortholog.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
   Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
   Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
   Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
   bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007831; AAK81274.1; -.
DR PIR; G97310; G97310.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
KW Complete proteome.
SQ SEQUENCE 292 AA; 31542 MW; 7EF0ECC9D59EED87 CRC64;

Query Match 54.5%; Score 109; DB 16; Length 292;
Best Local Similarity 62.5%; Pred. No. 5.5e-06;
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 9 GFIGTVMGKMGKINKLLKGGYTVHYVNRTEK 40

RESULT 14
Q97XZ7 PRELIMINARY; PRT; 289 AA.
ID Q97XZ7;
AC Q97XZ7;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Oxidoreductase.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;

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RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A., RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., RA Lauber J., Sjepeandic D., Hohnsels J., Straetz M., Helm S., RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B., RA Fraser C.M.;
 RA "Complete genome sequence and comparative analysis of the RT metabolically versatile *Pseudomonas putida* KT2440";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AE016778; AAN66768.1; -.
 DR TIGR; PF1143; -.
 DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006115; 6PGD.NAD.
 DR Pfam; PF03446; NAD_binding_2; 1.
 DR Complete proteome.
 KW SEQUENCE 295 AA; 30664 MW; 27E6E003982ED459 CRC64;
 SQ
 Query Match 48.0%; Score 96; DB 16; Length 295;
 Best Local Similarity 51.5%; Pred. No. 0.00027;
 Matches 17; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1 GFLGLMGSGIVSNLLKMGHTVTVWNRATK 33
 DB 9 GFAGTGLMGLEPCRRLLAAGYELTVWNRSPDK 41
 RESULT 21
 Q89HA0 PRELIMINARY; PRT; 313 AA.
 ID Q89HA0
 AC Q89HA0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Oxidoreductase.
 GN BLR6094.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., RA Tabata S.;
 RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium RT Bradyrhizobium japonicum USDA110";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005957; BACS1359.1; -.
 DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006183; 6PGD.
 DR Pfam; PF03446; NAD_binding_2; 1.
 DR PRINTS; PR00076; 6PGDHRGNASE.
 DR Complete proteome.
 KW SEQUENCE 313 AA; 32732 MW; 3B92612722105D51 CRC64;
 SQ

Query Match 48.0%; Score 96; DB 16; Length 313;
 Best Local Similarity 56.2%; Pred. No. 0.00029;
 Matches 18; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 GFLGLMGSGIVSNLLKMGHTVTVWNRATK 32
 DB 27 GYLGLMGTPMTRLLKAGQVSNRSEK 58

RESULT 22
 Q81S35

ID Q81S35 PRELIMINARY; PRT; 317 AA.
 AC Q81S35;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Dehydrogenase, putative.
 GN BAI842.
 OS *Bacillus anthracis* (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M., RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H., RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolisto A.-B., RA Fraser C.M.;
 RA "The genome sequence of *Bacillus anthracis* Ames and comparison to RT closely related bacteria";
 RL Nature 423:81-86(2003).
 DR EMBL; AE017029; AAP25747.1; -.
 DR TIGR; BAI842; -.
 DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006115; 6PGD.NAD.
 DR Pfam; PF03446; NAD_binding_2; 1.
 DR Complete proteome.
 KW SEQUENCE 317 AA; 33312 MW; CEA29415E4EF7A81 CRC64;
 SQ
 Query Match 48.0%; Score 96; DB 16; Length 317;
 Best Local Similarity 51.4%; Pred. No. 0.00029;
 Matches 18; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
 QY 3 LGLGLMGSGIVSNLLKMGHTVTVWNRATKCDLFI 37
 DB 35 IGLGPMGQALAGAFLMNGHPTTLWNRATKADYLI 69
 RESULT 23
 Q98GH7 PRELIMINARY; PRT; 475 AA.
 ID Q98GH7
 AC Q98GH7;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 6-phosphogluconate dehydrogenase.
 GN MLL3321.
 OS *Rhizobium loti* (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., RA Takeuchi C., Yamada M., Tabata S.;
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium RT Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003001; BABS0239.1; -.
 DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.

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DR InterPro; IPR008927; 6DGDH_C_like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006184; 6PGDm_BS.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD decarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding_2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR TIGRfams; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Complete proteome.
SQ SEQUENCE 475 AA; 50478 MW; DDCD80AE38E22DEE CRC64;

Query Match 48.0%; Score 96; DB 16; Length 475;
Best Local Similarity 42.1%; Pred. No. 0.00045;
Matches 16; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFIQ 38
Dd 7 GLIGLGTGMSNLALNIAEHGRIAVNRTAEKCDLFIQ 44

RESULT 24
Q82MW0 PRELIMINARY; PRT; 296 AA.
AC Q82MW0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative dehydrogenase.
GN SAV1542.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005027; BAC69253.1; -.
DR GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla...); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD binding_2; 1.
KW Complete proteome.
SQ SEQUENCE 296 AA; 30626 MW; 4A235B663CE97764 CRC64;

Query Match 46.5%; Score 93; DB 16; Length 296;
Best Local Similarity 50.0%; Pred. No. 0.00057;
Matches 16; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 3 LGFLMGSGIVSNLLKMGHTVTWNRRTAEKCD 34
Dd 10 LGTGINGAMARNLNAAGHTVAVNRTRAKAE 41

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RESULT 25
Q8FTI1 PRELIMINARY; PRT; 490 AA.
AC Q8FTI1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative 6-phosphogluconate dehydrogenase.
GN CE1588.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005219; BAC18398.1; -.
DR GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla...); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR008927; 6DGDH_C_like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006184; 6PGDm_BS.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD decarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding_2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR TIGRfams; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Complete proteome.
SQ SEQUENCE 490 AA; 53121 MW; BA20D7E0CDD86761 CRC64;

Query Match 46.5%; Score 93; DB 16; Length 490;
Best Local Similarity 45.9%; Pred. No. 0.0011;
Matches 17; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFI 37
Dd 17 GVUGLAVMGSLNARNFARNGHIVAVVNRSTDKLFI 53

RESULT 26
C05188 PRELIMINARY; PRT; 43 AA.
AC C05188;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative 6-phospho-gluconate dehydrogenase (Fragment).
GN ORF2.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98015408; PubMed=9353924;
RA Mueller J., Schiel S., Ordal G.W., Saxild H.H.;
RT "Functional and genetic characterization of mcpC, which encodes a
RT third methyl accepting chemotaxis protein in Bacillus subtilis.";
RL Microbiology 143:3231-3240(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93194799; PubMed=8449881;
RA Fajardo-Cavazos P., Salazar C., Nicholson W.L.;
RT "Molecular cloning and characterization of the Bacillus subtilis spore

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RT photoproduct lyase (spl) gene, which is involved in repair of UV
RT radiation-induced DNA damage during spore germination.;
RL J. Bacteriol. 175:1735-1744(1993).
DR EMBL; X97385; CAA66053.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphoglucuronate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
FT NON TR 43
FT SEQUENCE 43 AA; 4797 MW; 4E9F29DCB64945B CRC64;
SQ
Query Match 46.0%; Score 92; DB 2; Length 43;
Best Local Similarity 53.1%; Pred. No. 0.00012;
Matches 17; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 FLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
Db 6 GFGLGVMGKSMASHILNDGHPVLVYTRTKK 37
RESULT 27
Q7WFP7 PRELIMINARY; PRT; 301 AA.
ID Q7WFP7
AC Q7WFP7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative oxidoreductase.
GN BBA224.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640449; CAE34588.1; -.
KW Complete proteome.
SQ SEQUENCE 301 AA; 31326 MW; 91AC4FBF73F6925F CRC64;
Query Match 46.0%; Score 92; DB 16; Length 301;
Best Local Similarity 58.1%; Pred. No. 0.00091;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 2 FLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
Db 19 FLGLGVMLPAGHARAGHQVTVMNRTAAK 49
RESULT 28
Q7W489 PRELIMINARY; PRT; 302 AA.
ID Q7W489
AC Q7W489;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative oxidoreductase.
GN BP3779.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640434; CAE39062.1; -.
KW Complete proteome.
SQ SEQUENCE 302 AA; 31371 MW; B9696B7BAD09CA9D CRC64;
Query Match 46.0%; Score 92; DB 16; Length 302;
Best Local Similarity 58.1%; Pred. No. 0.00092;
Matches 18; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 2 FLGLGLMGSGIVSNLLKMGHTVTVMNRTAEK 32
Db 19 FLGLGVMLPAGHARAGHQVTVMNRTAAK 49
RESULT 29
Q9SZE1 PRELIMINARY; PRT; 334 AA.
ID Q9SZE1
AC Q9SZE1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Putative dehydrogenase).
GN F19B15.150 OR A14G29120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RC SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duisterhoef A.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duisterhoef A.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RC SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,

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RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A.A., Sena J.A.D., Silva C., de Souza R.P.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR ENBL; AE011657; AAM35214.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0006573; P-valine metabolism; IEA.
DR InterPro; IPR02204; 3hydroxoisobut.dh.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
KW Complete proteome.
SQ SEQUENCE 292 AA; 30453 MW; 4344A00544D44B8B CRC64;

Query Match          45.5%; Score 91; DB 16; Length 292;
Best Local Similarity 53.1%; Pred. NO. 0.0012;
Matches 17; Conservative 6; Mismatches 9; Indels 0; Gaps

Qy      1  GFGLGIMGSGIVSNLLKMGHTVTGVNNTAEK 32
        ||||| | : ||| : : ||| :
Db       4  GFGLGTMLGPNAHNLLRGGFALSVNRSRPER 35

Search completed: September 16, 2004, 07:45:56
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:28:53 ; Search time 59 Seconds
(without alignments)

2648.284 Million cell updates/sec

Title: US-10-067-482-2

Perfect score: 2866

Sequence: 1 MAVSLRLGLVWGLGRYP.....AKALDQSDMSAVRYAIIH 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2858	99.7	553	AA016415	AA016415 Human nuc
2	2811	98.1	547	AAW69240	AAW69240 Clone AQ7
3	2811	98.1	547	AAW69240	AAW69240 Human AQ7
4	2798	97.6	550	AAU21690	AAU21690 Novel hum
5	2798	97.6	550	ADC46331	ADC46331 Human neo
6	2396.5	83.6	472	AAE38240	AAE38240 Human enz
7	1404	49.0	269	AAU20515	AAU20515 Human sec
8	1404	49.0	269	AAU21813	AAU21813 Novel hum
9	1404	49.0	269	ADC46454	ADC46454 Human neo
10	1291	45.0	249	AAW09404	AAW09404 Human hep
11	1291	45.0	249	AAU09982	AAU09982 Human hep
12	1291	45.0	260	AAU20553	AAU20553 Human sec
13	1291	45.0	260	AAU21747	AAU21747 Novel hum
14	1286	44.9	250	AAU21590	AAU21590 Human neo
15	1286	44.9	250	AAU21590	AAU21590 Novel hum
16	1286	44.9	250	AAU21590	AAU21590 Novel hum
17	769.5	26.8	574	AAE19927	AAE19927 Drosophil
18	733	25.6	360	AAE19927	AAE19927 Corn 3-hy
19	720	25.1	290	AAE36391	AAE36391 Tulip pis
20	695	24.2	289	AAE36392	AAE36392 A. thalia
21	682	23.8	345	AAE19929	AAE19929 Soybean 3
22	679	23.7	289	AAE19491	AAE19491 Amino aci
23	667.5	23.3	353	AAE10423	AAE10423 Arabidops
24	667	23.3	343	AAE10424	AAE10424 Arabidops
25	629	21.9	285	AAE10425	AAE10425 Arabidops

26	537.5	18.8	5	AAE19926	Corn 3-hy
27	399	13.9	3	AAE19926	Arabidops
28	384	13.4	3	AAE19926	Arabidops
29	384	13.4	3	AAE19926	Arabidops
30	384	13.4	3	AAE19926	Arabidops
31	375	13.1	292	AAE19926	Arabidops
32	367	12.8	299	AAE19926	Arabidops
33	361	12.6	158	AAE19926	Arabidops
34	352	12.3	154	AAE19926	Arabidops
35	350	12.2	296	AAE19926	Arabidops
36	343.5	12.0	299	AAE19926	Arabidops
37	342	11.9	289	AAE19926	Arabidops
38	342	11.9	289	AAE19926	Arabidops
39	342	11.9	289	AAE19926	Arabidops
40	340	11.9	295	AAE19926	Arabidops
41	340	11.9	299	AAE19926	Arabidops
42	334.5	11.7	295	AAE19926	Arabidops
43	331	11.5	286	AAE19926	Arabidops
44	331	11.5	286	AAE19926	Arabidops
45	330	11.5	285	AAE19926	Arabidops
46	330	11.5	289	AAE19926	Arabidops
47	329	11.5	289	AAE19926	Arabidops
48	329	11.5	289	AAE19926	Arabidops
49	328	11.4	347	AAE19926	Arabidops
50	327.5	11.4	290	AAE19926	Arabidops
51	327.5	11.4	347	AAE19926	Arabidops
52	324.5	11.3	288	AAE19926	Arabidops
53	318	11.1	296	AAE19926	Arabidops
54	316	11.0	293	AAE19926	Arabidops
55	314.5	11.0	277	AAE19926	Arabidops
56	314	11.0	297	AAE19926	Arabidops
57	313.5	10.9	161	AAE19926	Arabidops
58	313.5	10.9	301	AAE19926	Arabidops
59	301.5	10.5	292	AAE19926	Arabidops
60	301.5	10.5	292	AAE19926	Arabidops
61	301.5	10.5	297	AAE19926	Arabidops
62	296.5	10.3	300	AAE19926	Arabidops
63	296.5	10.3	300	AAE19926	Arabidops
64	295	10.2	299	AAE19926	Arabidops
65	291.5	10.2	292	AAE19926	Arabidops
66	290.5	10.1	298	AAE19926	Arabidops
67	289.5	10.1	296	AAE19926	Arabidops
68	289.5	10.1	296	AAE19926	Arabidops
69	287.5	10.0	293	AAE19926	Arabidops
70	285	9.9	308	AAE19926	Arabidops
71	281	9.8	291	AAE19926	Arabidops
72	281	9.8	336	AAE19926	Arabidops
73	281	9.8	336	AAE19926	Arabidops
74	281	9.8	336	AAE19926	Arabidops
75	279.5	9.8	292	AAE19926	Arabidops
76	279.5	9.8	302	AAE19926	Arabidops
77	278.5	9.7	324	AAE19926	Arabidops
78	277	9.7	302	AAE19926	Arabidops
79	272.5	9.5	292	AAE19926	Arabidops
80	272	9.5	288	AAE19926	Arabidops
81	269	9.4	297	AAE19926	Arabidops
82	266	9.3	326	AAE19926	Arabidops
83	258.5	9.0	342	AAE19926	Arabidops
84	250.5	8.7	158	AAE19926	Arabidops
85	250.5	8.7	180	AAE19926	Arabidops
86	250.5	8.7	182	AAE19926	Arabidops
87	248.5	8.7	287	AAE19926	Arabidops
88	240.5	8.4	350	AAE19926	Arabidops
89	235	8.2	287	AAE19926	Arabidops
90	234.5	8.2	294	AAE19926	Arabidops
91	214.5	7.5	551	AAE19926	Arabidops
92	209	7.3	426	AAE19926	Arabidops
93	199.5	7.0	305	AAE19926	Arabidops
94	193	6.7	475	AAE19926	Arabidops
95	190.5	6.6	202	AAE19926	Arabidops
96	189	6.6	203	AAE19926	Arabidops
97	189	6.6	203	AAE19926	Arabidops
98	189	6.6	203	AAE19926	Arabidops

99 189 6.6 203 4 AAB70073 Human sec
100 189 6.6 203 4 AAB92800 Human pro

ALIGNMENTS

RESULT 1
ID AAO16415 standard; protein; 553 AA.
AC AAO16415;
DT 10-APR-2003 (first entry)
DE Human nucleic acid-associated protein (NAAP) - SEQ ID No 12.
KW Human; nucleic acid-associated protein; NAAP; arteriosclerosis;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;
KW cancer; developmental disorder; renal tubular acidosis; anaemia; asthma;
KW mental retardation; neurological disorder; Alzheimer's disease; epilepsy;
KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;
KW Crohn's disease; transgenic animal; animal model.
OS Homo sapiens.
PN WO2003000864-A2.
PD 03-JAN-2003.
PF 20-JUN-2002; 2002WO-US021179.
PR 22-JUN-2001; 2001US-0300518P.
PR 29-JUN-2001; 2001US-0301787P.
PR 29-JUN-2001; 2001US-0301792P.
PR 29-JUN-2001; 2001US-0301892P.
PR 29-JUN-2001; 2001US-0301893P.
PR 06-JUL-2001; 2001US-0303405P.
PR 06-JUL-2001; 2001US-0303442P.
PR 15-MAR-2002; 2002US-0364438P.
PA (INCYTE) INCYTE GENOMICS INC.
XX Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM;
XX Arvizu CS, Ison CH, Honchell CB, Lee EA, Yue H, Forsythe IJ;
XX Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MK;
XX Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha SD, Lee SY;
XX Richardson TW, Elliott VS, Luo W, Tang YT, Zebardjian Y, Lu Y;
XX WPT; 2003-201420/19.
XX N-PSDE; AAL51565.
XX New nucleic acid-associated proteins and polynucleotides, useful for
XX diagnosing, treating or preventing cell proliferative (e.g. cancer),
XX neurological (e.g. epilepsy or Parkinson's disease), or autoimmune
XX disorders (e.g. AIDS).
XX Claim 1; Page 227-228; 312pp; English.
XX The invention comprises the amino acid and coding sequences of human
XX nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
XX the invention are useful for diagnosing, treating or preventing disorders
XX associated with aberrant expression of NAAP, such as: cell proliferative
XX disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis
XX or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia
XX or mental retardation); neurological disorders (e.g. Alzheimer's disease,
XX Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders
XX (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of
XX the invention are useful for creating transgenic animals to model human
XX disease. The present amino acid sequence represents a human nucleic acid-
XX associated protein of the invention
XX Sequence 553 AA;

Query Match 99.7%; Score 2858; DB 6; Length 553;
Best Local Similarity 99.8%; Pred. No. 2.7e-254;
Matches 552; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAVSLRLGDLVWGLGRYPWPWPKIVNPPDKKPRGKKCFVFFFGTDEHAWIKVEQL 60
DB 1 MAAVSLRLGDLVWGLGRYPWPWPKIVNPPDKKPRGKKCFVFFFGTDEHAWIKVEQL 60

QY 61 KPYHAKGEMIKINGKRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSERSRP 120
DB 61 KPYHAKGEMIKINGKRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSERSRP 120

QY 121 NSGDEKRLKLSLEGKVKKNMGEGKRVSSGSGSERGSKPLKRAQEQSPKRGPPKDEKD 180
DB 121 NSGDEKRLKLSLEGKVKKNMGEGKRVSSGSGSERGSKPLKRAQEQSPKRGPPKDEKD 180

QY 181 LTIPESSTVKGMAGPMAAFKWPQTASEPVKQADPHFHLFSQTEKPAVCYQAITKKLK 240
DB 181 LTIPESSTVKGMAGPMAAFKWPQTASEPVKQADPHFHLFSQTEKPAVCYQAITKKLK 240

QY 241 ICEEETGTSIOAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTA 300
DB 241 ICEEETGTSIOAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTA 300

QY 301 EKCDLFIQEGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDM 360
DB 301 EKCDLFIQEGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDM 360

QY 361 STVDADTVTELAQVIIVSRGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 420
DB 361 STVDADTVTELAQVIIVSRGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 420

QY 421 GKTSFFLGEVGNAAKMLIVNMVQGSFMATIAEGLTLAHTVGTQSQTLLDLNQGQLASI 480
DB 421 GKTSFFLGEVGNAAKMLIVNMVQGSFMATIAEGLTLAHTVGTQSQTLLDLNQGQLASI 480

QY 481 FLDPKQCNILQGNFKPDFVLYKIQKDLRLAIALGDVNHPTPMAAAANEVYKRAKALDOS 540
DB 481 FLDPKQCNILQGNFKPDFVLYKIQKDLRLAIALGDVNHPTPMAAAANEVYKRAKALDOS 540

QY 541 DNDMSAVRYAYIH 553
DB 541 DNDMSAVRYAYIH 553

RESULT 2
ID AAW69240 standard; protein; 547 AA.
XX AAW69240;
XX AC AAW69240;
XX DT 21-OCT-1998 (first entry)
XX DE Clone AQ73_3 protein sequence.
XX KW Secreted protein; nutritional source; cell proliferation activity;
XX KW cell differentiation activity; immune stimulant; tissue growth activator;
XX KW haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor;
XX KW tumour inhibitor; clone AQ73_3.
XX OS Homo sapiens.
XX PN WO9825962-A2.
XX PD 18-JUN-1998.
XX PF 12-DEC-1997; 97WO-US023224.
XX PR 13-DEC-1996; 96US-00766263.
XX PR 11-DEC-1997; 97US-00989232.
XX PA (GEM) GENETICS INST INC.

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XX  Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI  Spaulding V, Agostino MJ;
XX  WPI; 1998-362424/31.
DR  N-PSDB; AAV44859.
XX  New isolated polynucleotides - obtained from human adult testis, human
PT  adult ovary, human adult brain and human adult heart cDNA libraries.
XX  Claim 15; Page 66-67; 108pp; English.
XX  This sequence is secreted protein, encoded by a polynucleotide of the
CC  invention. The DNA was isolated from a human adult ovary cDNA library,
CC  and is designated clone AQ73_3. The DNA sequences and encoded
CC  polypeptides can be used as nutritional sources or supplements, or may
CC  exhibit e.g. cytokine and cell proliferation/differentiation activity,
CC  immune stimulating or suppressing activity, haematopoiesis regulating
CC  activity, receptor/ligand activity, anti-inflammatory activity,
CC  activin/inhibin activity, chemostatic/chemokinetic activity,
CC  cadherin/tumour invasion suppressor activity, tissue growth activity,
CC  tumour inhibition activity or other activities
XX  Sequence 547 AA;
XX  Query Match
PI  Best Local Similarity 98.1%; Score 2811; DB 2; Length 547;
PI  Matches 546; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
XX  QY 1 MAASVLRGLDVLWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKGFGTEHAWIKVEQL 60
DB 1 MAASVLRGLDVLWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKGFGTEHAWIKVEQL 60
XX  QY 61 KPYHAHKEIMIKINKGRFQQQAVDAVEEFLRAKGDQTSNHSDDKNRRNSSEERSRP 120
DB 61 KPYHAHKEIMIKINKGRFQQQAVDAVEEFLRAKGDQTSNHSDDKNRRNSSEERSRP 120
XX  QY 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSGSGSERGSKSPLKRAQSQSPRKRGRPPKDEKD 180
DB 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSGSGSERGSKSPLKRAQSQSPRKRGRPPKDEKD 180
XX  QY 181 LTIPESSVTKGMMAGPMAAFKWPQTAASEPVKDADPHHFLLSQTEKPAVCYQAITKKLK 240
DB 181 LTIPESSVTKGMMAGPMAAFKWPQTAASEPVKDADPHHFLLSQTEKPAVCYQAITKKLK 240
XX  QY 241 ICEBETGSTSIQAADSTAVNGSIITPDKKIGLGLMGSGIVSNLLKMGHTVTVNNRTA 300
DB 241 ICEBETGSTSIQAADSTAVNGSIITPDKKIGLGLMGSGIVSNLLKMGHTVTVNNRTA 300
XX  QY 301 EKCDLFIQEGARLGRTPAEVVSVCITITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 360
DB 301 EK-----EGARLGRTPAEVVSVCITITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 360
XX  QY 361 STVDADITVTELAQVIVSRGGRFLAPVSGNOOLNDGMLVILAGDRLGEDSCSCFOAM 420
DB 361 STVDADITVTELAQVIVSRGGRFLAPVSGNOOLNDGMLVILAGDRLGEDSCSCFOAM 420
XX  QY 421 KGTSTFFLGEVGNAAKMLIVNMVQGSFMATIAEGLTLAHTVGTQSQQTLLDILNOGQLASI 480
DB 421 KGTSTFFLGEVGNAAKMLIVNMVQGSFMATIAEGLTLAHTVGTQSQQTLLDILNOGQLASI 480
XX  QY 481 FLDOCKQNILOGNFKPDPFLKYIKQDLRLAIALGDVANNHPTPMAAANEVYKRAKALDQS 540
DB 481 FLDOCKQNILOGNFKPDPFLKYIKQDLRLAIALGDVANNHPTPMAAANEVYKRAKALDQS 540
XX  QY 541 DNDMSAVYRAYIH 553
DB 541 DNDMSAVYRAYIH 547
XX  QY 535 DNDMSAVYRAYIH 547

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RESULT 3
AAB90720
ID AAB90720

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XX  AAB90720;
XX  07-JUN-2001 (first entry)
XX  Human AQ73_3 protein sequence SEQ ID 137.
XX  Human; secreted protein; nutrient; cytokine modulator; proliferation;
XX  differentiation; immune system modulator; tissue growth; chemotactic;
XX  haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
XX  haematopoiesis.
XX  Homo sapiens.
XX  WO200119988-A1.
XX  22-MAR-2001.
XX  14-SEP-2000; 2000WO-US025135.
XX  17-SEP-1999; 99US-00398829.
XX  (GEMY ) GENETICS INST INC.
XX  Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX  Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX  WPI; 2001-244801/25.
XX  N-PSDB; AAF98456.
XX  Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
XX  cytokine and cell proliferation/differentiation activity, the immune
XX  system and hematopoiesis regulating activity.
XX  Disclosure; Page 468-470; 557pp; English.
XX  Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
XX  proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
XX  tissue types, and may be used in the prevention, treatment and diagnosis
XX  of diseases associated with inappropriate protein expression. The
XX  polypeptides and nucleic acids may be used as nutrients or to modulate
XX  cytokine and cell proliferation/differentiation activity and may also be
XX  involved in modulation of the immune system. The cDNA sequences,
XX  proteins, their agonists and/or antagonists exhibit haematopoiesis
XX  regulating activity; tissue growth activity; activin/inhibin activity;
XX  chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
XX  receptor/ligand activity; anti-inflammatory activity; haematopoiesis
XX  activity; cadherin/tumour suppressor activity; and/or tumour inhibition
XX  activity. Included in the invention are probes represented in AAF98490 -
XX  AAF98572 which are specific for the cDNA clones encoding the secreted
XX  proteins
XX  Sequence 547 AA;
XX  Query Match
XX  Best Local Similarity 98.1%; Score 2811; DB 4; Length 547;
XX  Matches 546; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
XX  QY 1 MAASVLRGLDVLWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKGFGTEHAWIKVEQL 60
DB 1 MAASVLRGLDVLWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKGFGTEHAWIKVEQL 60
XX  QY 61 KPYHAHKEIMIKINKGRFQQQAVDAVEEFLRAKGDQTSNHSDDKNRRNSSEERSRP 120
DB 61 KPYHAHKEIMIKINKGRFQQQAVDAVEEFLRAKGDQTSNHSDDKNRRNSSEERSRP 120
XX  QY 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSGSGSERGSKSPLKRAQSQSPRKRGRPPKDEKD 180
DB 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSGSGSERGSKSPLKRAQSQSPRKRGRPPKDEKD 180
XX  QY 181 LTIPESSVTKGMMAGPMAAFKWPQTAASEPVKDADPHHFLLSQTEKPAVCYQAITKKLK 240
DB 181 LTIPESSVTKGMMAGPMAAFKWPQTAASEPVKDADPHHFLLSQTEKPAVCYQAITKKLK 240

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us-10-067-482-2.rag

QY	241	ICEETGTSIQADSTAVNGSITPTDKKIGFLGLMGSGIVSNLLKMGHTVTVWNRTA	300
DB	241	ICEETGTSIQADSTAVNGSITPTDKKIGFLGLMGSGIVSNLLKMGHTVTVWNRTA	300
QY	301	EKCDLFIQEGARLGTAEVSTCDITFACVSDPKAAKDLVLGPGSVLQGIIRPGKCYVDM	360
DB	301	EK-----EGARLGTAEVSTCDITFACVSDPKAAKDLVLGPGSVLQGIIRPGKCYVDM	354
QY	361	STVDADTVTELAAQVIVSRGRLEAPVSGNQQLSNDGMLVILAAAGRGLYEDCSCFQAM	420
DB	355	STVDADTVTELAAQVIVSRGRLEAPVSGNQQLSNDGMLVILAAAGRGLYEDCSCFQAM	414
QY	421	GKTSFPLGEVGNAAKMWLVNVMVQGSFMATIAEGLTLAHTGQSQTLLDILNQGLAST	480
DB	415	GKTSFPLGEVGNAAKMWLVNVMVQGSFMATIAEGLTLAHTGQSQTLLDILNQGLAST	474
QY	481	FLDQKQNTLQGNFKPDFLYIKYIKDLRLAIALGDVNHPTMAAANAEVYKRAKALDOS	540
DB	475	FLDQKQNTLQGNFKPDFLYIKYIKDLRLAIALGDVNHPTMAAANAEVYKRAKALDOS	534
QY	541	DNDMSAVYRAYIH 553	
DB	535	DNDMSAVYRAYIH 547	
RESULT 4			
AAU21690			
ID	AAU21690 standard; protein; 550 AA.		
AC	AAU21690;		
DT	04-DEC-2001 (first entry)		
XX	Novel human neoplastic disease associated polypeptide #123.		
KW	Human; neoplastic disease associated polypeptide; cancer;		
KW	hyperproliferative disorder; neural disorder; immune system disorder;		
KW	muscular disorder; reproductive disorder; gastrointestinal disorder;		
KW	pulmonary disorder; cardiovascular disorder; renal disorder;		
KW	neuroprotective; cytostatic; anti inflammatory; vasotropic.		
OS	Homo sapiens.		
XX	WO200155163-A1.		
PD	02-AUG-2001.		
XX	17-JAN-2001; 2001WO-US001358.		
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076P.		
PR	18-APR-2000; 2000US-0198123P.		
PR	19-MAY-2000; 2000US-0205515P.		
PR	07-JUN-2000; 2000US-0209467P.		
PR	28-JUN-2000; 2000US-0214886P.		
PR	30-JUN-2000; 2000US-0215135P.		
PR	07-JUL-2000; 2000US-0216647P.		
PR	07-JUL-2000; 2000US-0216880P.		
PR	11-JUL-2000; 2000US-0217487P.		
PR	11-JUL-2000; 2000US-0217496P.		
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PR	22-AUG-2000;	2000US-0227183P.
PR	23-AUG-2000;	2000US-0227009P.
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PR	06-SEP-2000;	2000US-0230437P.
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PR	08-SEP-2000;	2000US-0231242P.
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PR	08-SEP-2000;	2000US-0231414P.
PR	08-SEP-2000;	2000US-0232080P.
PR	08-SEP-2000;	2000US-0232081P.
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PR	21-SEP-2000;	2000US-0234223P.
PR	21-SEP-2000;	2000US-0234274P.
PR	25-SEP-2000;	2000US-0234997P.
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PR	26-SEP-2000;	2000US-0235484P.
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PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239935P.
PR	13-OCT-2000;	2000US-0239937P.
PR	20-OCT-2000;	2000US-0240960P.
PR	20-OCT-2000;	2000US-0241221P.
PR	20-OCT-2000;	2000US-0241785P.
PR	20-OCT-2000;	2000US-0241786P.
PR	20-OCT-2000;	2000US-0241787P.
PR	20-OCT-2000;	2000US-0241809P.
PR	20-OCT-2000;	2000US-0241826P.
PR	01-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
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PR	08-NOV-2000;	2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
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 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
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 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
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 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
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 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2001US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-465558/50.
 N-PSDB; AAS34889.
 Novel polypeptides and polynucleotides useful as diagnostic reagents to
 diagnose diseases or disorders associated with aberrant expression or
 activity of polypeptides, and for treating cancers, rheumatoid arthritis.
 Claim 11; SEQ ID NO 417; 687pp; English.
 The present invention relates to the isolation of novel human neoplastic
 disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA
 sequences encoding for these polypeptides. The sequences of the invention
 are useful in the diagnosis, treatment, prevention and/or prognosis of
 disorders involving neoplastic disease such as hyperproliferative
 disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
 glioma, adult liver cancer, childhood cerebellar astrocytoma, or
 Hodgkin's lymphoma). The sequences of the invention may also be useful
 for treating other disorders such as neural disorders, immune system
 disorders, muscular disorders, reproductive disorders, gastrointestinal
 disorders, pulmonary disorders, cardiovascular disorders and renal
 disorders. The polynucleotide sequences of the invention are also useful
 in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
 disease associated polypeptides of the invention. Note: The sequence data
 for this patent did not form part of the invention. Note: The sequence data
 obtained in electronic format directly from the printed specification, but was
 ftp.wipo.int/pub/published_sequences

Sequence 550 AA;

Query Match 97.6%; Score 2798; DB 4; Length 550;
 Best Local Similarity 98.7%; Pred. No. 9.3e-249;
 Matches 543; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
 QY 4 VSLRLGDLVWGKLGKRYPPWPGKIVNPPKDLKKPKGKCKFFVKFGTETHAIKVEQLKPY 63
 DB 7 VSLRLGDLVWGKLGKRYPPWPGKIVNPPKDLKKPKGKCKFFVKFGTETHAIKVEQLKPY 66
 QY 64 HAHKEEMIKINKGRFOQAVDAVEEFLRRRAKQDQTSNNSDDKNRNSSEERSRNSG 123
 DB 67 HAHKEEMIKINKGRFOQAVDAVEEFLRRRAKQDQTSNNSDDKNRNSSEERSRNSG 126
 QY 124 DEKKLSLSEGGYKKNMGEKKRVSSESSSRRGSKSPKRAQEQSPKRGKRPKDEKDLTI 183
 DB 127 DEKKLSLSEGGYKKNMGEKKRVSSESSSRRGSKSPKRAQEQSPKRGKRPKDEKDLTI 186
 QY 184 PESSTVKGMMAGPMAAFKWOPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLICE 243
 DB 187 PESSTVKGMMAGPMAAFKWOPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLICE 246
 QY 244 EETGSTSIOAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEK 303
 DB 247 EETGSTSIOAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEK - 305
 QY 304 DLFIQEGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGSPGVLOQIRPGKCYDMSTV 363
 DB 306 -----EGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGSPGVLOQIRPGKCYDMSTV 360
 QY 364 DADTVTELAQVIVSRGRFLEAPVSGNQOLSDNGLMVLIAAGDRGLYEDCSSCFQAMGT 423
 DB 361 DADTVTELAQVIVSRGRFLEAPVSGNQOLSDNGLMVLIAAGDRGLYEDCSSCFQAMGT 420
 QY 424 SPFLGEVGNAAKMLIVNVVQGSFMATIAEGLTIAHVTGSSQOTLLDILNQGLASIFLD 483
 DB 421 SPFLGEVGNAAKMLIVNVVQGSFMATIAEGLTIAHVTGSSQOTLLDILNQGLASIFLD 480
 QY 484 QKCONILOGNFKPDPFYLYIKQDLRLAIALGDVAVNHTPMAAANVYKRAKALDQSDND 543
 DB 481 QKCONILOGNFKPDPFYLYIKQDLRLAIALGDVAVNHTPMAAANVYKRAKALDQSDND 540
 QY 544 MSAYVRAYTH 553
 DB 541 MSAYVRAYTH 550
 RESULT 5
 ADC46331
 ID ADC46331 standard; protein; 550 AA.
 XX AC ADC46331;
 XX AC ADC46331;
 DT 18-DEC-2003 (first entry)
 XX Human neoplastic disease-associated gene 123 protein #1.
 DE Neoplastic disease-associated polypeptide; gene therapy;
 XX hyperproliferative disease; cancer; autoimmune disorder; diabetes;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
 KW haematologic disorder; anaemia; thrombocytopenia; allergic reaction;
 KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
 KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; renal disorder;
 KW acute glomerulonephritis; end-stage renal disease;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; AIDS; cachexia; anorexia; wound healing;
 KW epithelial cell proliferation; Human.
 XX Homo sapiens.
 OS
 XX
 PN US2003082758-A1.
 XX

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PD 01-MAY-2003.
XX
XX
XX
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PR 22-MAR-2002; 2002US-00103313.
PR
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PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
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PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
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(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM, Barash SC;
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61 KPYHAKEIMKNGKRFQQAQVDAVEEFLRRAKGDQ-----98

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QY	121	NSGDEKRLSLSEGVKKQNMGEKRVSSGSSERGSKPLKRAQEOSPKRGPPKDEKD	180
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QY	241	ICBEETGTSIOAADSTAVNGSITPTDKKIGFLGLGMSGGIVSNLLKMGHTVTVMNR	300
Db	160	ICBEETGTSIOAADSTAVNGSITPTDKKIGFLGLGMSGGIVSNLLKMGHTVTVMNR	219
QY	301	EKCDLFIQEGARLGRTPAEVWSTCDITFACVSPKAAKDLVLPSPGVQIRPGKCYVDM	360
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QY	361	STVDADTVTELAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM	420
Db	280	STVDADTVTELAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM	339
QY	421	GKTSFFLGEVGNAAKMMLIYNNVQGSFMTIAEGLTLAHTVQSGQOTLLDILNQGLASI	480
Db	340	GKTSFFLGEVGNAAKMMLIYNNVQGSFMTIAEGLTLAHTVQSGQOTLLDILNQGLASI	399
QY	481	FLDQKQNILQGNPKPDFYLYIKQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS	540
Db	400	FLDQKQNILQGNPKPDFYLYIKQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS	459
QY	541	DNDMSAVYRAYIH	553
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XX	DT	06-DEC-2001 (first entry)	
XX	DE	Human secreted protein, Seq ID No 507.	
XX	KW	Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;	
XX	KW	rheumatoid arthritis; antiarteriosclerotic; cardiac; vascular;	
XX	KW	cerebroprotective; thrombolytic; antimicrobial; ophthalmological;	
XX	KW	cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer;	
XX	KW	multiple sclerosis; cancer; hyperproliferative disorder; infection;	
XX	KW	Gaucher's disease; neurological disease; cerebrovascular disorder;	
XX	OS	thrombosis; wound healing.	
XX	OS	Homo sapiens.	
XX	PN	WO200155326-A2.	
XX	PD	02-AUG-2001.	
XX	PF	17-JAN-2001; 2001WO-US001347.	
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 (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-451931/48.
 DR N-PSDB; AAS33224.
 XX
 PT New nucleic acids and polypeptides, useful for diagnosing, preventing or
 XX treating medical conditions.
 PS Claim 11; SEQ ID NO 507; 753pp; English.
 XX
 CC The invention relates to novel isolated nucleic acid molecules (I)
 CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
 CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
 CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
 CC the prevention, treatment and diagnosis of diseases associated with
 CC inappropriate expression of secreted proteins. (I) and complementary
 CC sequences may also be used as DNA probes in diagnostic assays (e.g.
 CC polymerase chain reactions (PCR)) to detect and quantitate the presence
 CC of similar nucleic acid sequences in samples, and so which patients may
 CC be in need of restorative therapy. (II) may also be used as antigens in

CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of the secreted
 CC proteins. The anti-(II) antibodies and antagonists may also be used to
 CC down regulate expression and activity of (II). The anti-(II) antibodies
 CC may also be used as diagnostic agents for detecting the presence of (II)
 CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
 CC disorders include for example: immune/ autoimmune diseases (e.g. HIV
 CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
 CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
 CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
 CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
 CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and
 CC thrombosis), infections caused by bacteria, viruses and fungi and ocular
 CC disorders (e.g. corneal infections). (I) and (II), agonists, antagonists
 CC and antibodies can also be used to promote wound healing, maintain organs
 CC before transplantation, and support cell culture of primary tissues.

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 Matches 267; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 QY 64 HAHKEEMIKINKGRFQQAQVDAVEEFLRAKQDQTSNHSDDKNNRNSERSRNSG 123
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RESULT 8

AAU21813
 ID AAU21813 standard; protein; 269 AA.

XX
 AC AAU21813;

XX
 DT 06-DEC-2001 (first entry)

XX
 DE Novel human neoplastic disease associated polypeptide #246.

XX Human; neoplastic disease associated polypeptide; cancer;
 KW hyperproliferative disorder; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW neuroprotective; cytostatic; anti inflammatory; vasotropic.

XX Homo sapiens.

XX WO200155163-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US0001358.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

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PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
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PR 05-DEC-2000; 2000US-0251030P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-465558/50.
DR N-PSDB; AAS35012.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
XX Claim 11; SEQ ID NO 540; 687pp; English.
PS
XX The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA

CC sequences encoding for these polypeptides. The sequences of the invention
 CC are useful in the diagnosis, treatment, prevention and/or prognosis of
 CC disorders involving neoplastic disease such as hyperproliferative
 CC disorders (e.g. leukemia, bone cancer, bladder cancer, brain stem
 CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or
 CC Hodgkin's lymphoma). The sequences of the invention may also be useful
 CC for treating other disorders such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, pulmonary disorders, cardiovascular disorders and renal
 CC disorders. The polynucleotide sequences of the invention are also useful
 CC in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
 CC disease associated polypeptides of the invention. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 269 AA;

Query Match 49.0%; Score 1404; DB 4; Length 269;
 Best Local Similarity 99.3%; Pred. No. 1.3e-120;
 Matches 267; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 VSLRLGDLVWGLGRYPWPFGKIVNPPKDLKKPRGKKCPVKEFCTEDHAWIKVEQLKPY 63
 Db 1 VSLRLGDLVWGLGRYPWPFGKIVNPPKDLKKPRGKKCPVKEFCTEDHAWIKVEQLKPY 60
 QY 64 HAHKEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKRNSSERSRPNNG 123
 Db 61 HAHKEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKRNSSERSRPNNG 120
 QY 124 DEKRKLSLSEGVKKMGKGRVSSGSSERGSKSPKRAEQSPKRGPRPPKDEKDLTI 183
 Db 121 DEKRKLSLSEGVKKMGKGRVSSGSSERGSKSPKRAEQSPKRGPRPPKDEKDLTI 180
 QY 184 PSSVTVKMGMAFPMAFKWQPTASEVPKADDPHFHLLSOTEKPAVCYQATTKLKICE 243
 Db 181 PSSVTVKMGMAFPMAFKWQPTASEVPKADDPHFHLLSOTEKPAVCYQATTKLKICE 240
 QY 244 BETGSTSIQAADSTAVNGSIITPDKKIGF 272
 Db 241 BETGSTSIQAADSTAVNGSIITPDKKIGF 269

RESULT 9

ID ADC46454
 AC ADC46454 standard; protein; 269 AA.

AC ADC46454;

DT 18-DEC-2003 (first entry)

DE Human neoplastic disease-associated gene 123 protein #2.

XX Neoplastic disease-associated polypeptide; gene therapy;
 KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
 KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
 KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
 KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; renal disorder;
 KW acute glomerulonephritis; end-stage renal disease;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; AIDS; cachexia; anorexia; wound healing;
 KW epithelial cell proliferation; Human.

OS Homo sapiens.

XX US2003082758-A1.

PN 01-MAY-2003.

XX 22-MAR-2002; 2002US-00103313.

XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
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 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
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 PR 14-AUG-2000; 2000US-0225268P.
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 PR 29-SEP-2000; 2000US-0236327P.
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 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.

XX 05-JUN-1995; 95WO-US0006731.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Kunsch CA, Rosen CA;
 PI WPI; 1997-043108/04.
 DR N-PSDB; AAT47520.
 XX DNA encoding human-derived growth factor polypeptide - useful to promote
 XX wound healing as result of burns or ulcers.
 PT Claim 7; Fig 2; 54pp; English.
 PS
 XX Human hepatoma-derived growth factor-2 (HDGF-2) (AAM09404) shows 23%
 CC identity and 61% similarity over a 201-amino acid stretch to human HDGF,
 CC a mitogen for fibroblasts. Its amino acid sequence was deduced from a
 CC cDNA clone (AAT47520) isolated from a human umbilical vein endothelial
 CC tissue cDNA library. Recombinant HDGF-2 can be produced in transformed
 CC host (e.g. E. coli, Sf9, COS) cells. It is useful in stimulating tissue
 CC repair and tissue growth and can also be used to produce antibodies and
 CC to screen for antagonists that retard tumour growth and reduce scarring
 XX
 SQ Sequence 249 AA;
 Query Match 45.0%; Score 1291; DB 2; Length 249;
 Best Local Similarity 99.6%; Pred. No. 3e-110;
 Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAASLRGLDVLWGKLGKRYPPWPKIWNPPKOLKPRGKKCFVFKFGTDEHAWIKVEQL 60
 Db 1 MAASLRGLDVLWGKLGKRYPPWPKIWNPPKOLKPRGKKCFVFKFGTDEHAWIKVEQL 60
 QY 61 KPYHAHEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKNNRNSSESRP 120
 Db 61 KPYHAHEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKNNRNSSESRP 120
 QY 121 NSGDEKRLSLSEGKVKKNMGKRRVSSGSSGSRGSKPLKRAQESPKRGRPPPKDEKD 180
 Db 121 NSGDEKRLSLSEGKVKKNMGKRRVSSGSSGSRGSKPLKRAQESPKRGRPPPKDEKD 180
 QY 181 LTIPSSIVKGMAGPMFAFKWQPTASEPVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240
 Db 181 LTIPSSIVKGMAGPMFAFKWQPTASEPVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240
 QY 241 ICEE 244
 Db 241 ICED 244
 RESULT 11
 ABU09982
 ID ABU09982 standard; protein; 249 AA.
 AC ABU09982;
 XX
 XX 30-JUL-2003 (first entry)
 DT
 XX Human hepatoma-derived growth factor 2 (HDGF-2).
 DE
 XX Human; hepatoma-derived growth factor-2; HDGF-2; vasotropic; vulnery;
 KW nootropic; neuroprotective; antiparkinsonian; cytostatic;
 KW antiinflammatory; gene therapy; vascular endothelial cell growth;
 KW re-vascularisation; ischaemic tissue; thrombosis; arteriosclerosis;
 KW cardiovascular condition; mesodermal induction; limb regeneration;
 KW wound healing; injury; burn; surgery; ulcer; neuronal growth;
 KW neuronal damage; neuronal disorder; neuro-degenerative condition;
 KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;
 KW chondrocyte growth; bone regeneration; periodontal regeneration;
 KW tissue transplant; bone graft; skin aging; sunburn; keratinocyte growth;
 KW hair loss; hair-forming cell activation; melanocyte growth;
 KW haematopoietic cell growth; haematopoietic cell differentiation;

KW bone marrow cell; organ transplantation; mesodermal tissue; cell growth;
 KW cell proliferation; tumour; hypervascular disease;
 KW epithelial lens cell proliferation; extracapsular cataract surgery;
 KW restenosis; balloon angioplasty; inflammation; scar tissue.
 XX Homo sapiens.
 OS
 XX US2003022312-A1.
 PN
 XX 30-JAN-2003.
 PD
 XX 15-NOV-2001; 2001US-00987755.
 PF
 XX 05-JUN-1995; 95US-00464600.
 PR 05-MAR-1999; 99US-00263625.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Kunsch CA, Rosen CA;
 XX WPI; 2003-447425/42.
 DR N-PSDB; ACA61586.
 XX

Novel isolated human hepatoma-derived growth factor-2 polypeptide useful
 PT for promoting healing in wounds, treating or prevention of Alzheimer's
 PT disease, stimulating chondrocyte growth, preventing skin aging, and
 PT preventing hair loss.
 XX Claim 2; Fig 1; 21pp; English.

XX The invention describes a polypeptide (I) having a deduced amino acid
 CC sequence of human hepatoma-derived growth factor-2 (HDGF-2) polypeptide
 CC sequence of 249 amino acids (S2) as given in the specification, or its
 CC fragments, analogues or derivatives. (I) is useful for stimulating
 CC vascular endothelial cell growth, and thus is employed in treating for
 CC stimulating re-vascularisation of ischaemic tissues due to various
 CC disease conditions such as thrombosis, arteriosclerosis, and other
 CC cardiovascular conditions; stimulating mesodermal induction and limb
 CC regeneration in early embryos; promoting healing in wounds due to
 CC injuries, burns, surgery, and ulcers; stimulating neuronal growth, and
 CC thus for treating or preventing neuronal damage occurring in certain
 CC neuronal disorders or neuro-degenerative conditions such as Alzheimer's
 CC disease, Parkinson's disease, and AIDS-related complex; stimulating
 CC chondrocyte growth and thus for enhancing bone and periodontal
 CC regeneration, and aiding in tissue transplants or bone grafts; preventing
 CC skin aging due to sunburn by stimulating keratinocyte growth; preventing
 CC hair loss by activating hair-forming cells and promoting melanocyte
 CC growth; stimulating growth and differentiation of haematopoietic cells
 CC and bone marrow cells; maintaining organs before transplantation; and
 CC inducing tissue of mesodermal origin to differentiate in early embryos.
 CC The antagonists of (I) are useful for inhibiting the cell growth and
 CC proliferation effects of the polypeptides on neoplastic cells and
 CC tissues, and therefore are useful for preventing abnormal cellular growth
 CC and proliferation e.g. in tumour formation or growth; preventing
 CC hypervascular diseases and preventing the proliferation of epithelial
 CC lens cells after extracapsular cataract surgery; preventing restenosis
 CC after balloon angioplasty; and preventing inflammation and growth of scar
 CC tissue during wound healing. This is the amino acid sequence of human
 CC hepatoma-derived growth factor-2 (HDGF-2)

XX Sequence 249 AA;

Query Match 45.0%; Score 1291; DB 6; Length 249;
 Best Local Similarity 99.6%; Pred. No. 3e-110;
 Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAASLRGLDVLWGKLGKRYPPWPKIWNPPKOLKPRGKKCFVFKFGTDEHAWIKVEQL 60
 Db 1 MAASLRGLDVLWGKLGKRYPPWPKIWNPPKOLKPRGKKCFVFKFGTDEHAWIKVEQL 60
 QY 61 KPYHAHEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKNNRNSSESRP 120
 Db 61 KPYHAHEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHSDDKNNRNSSESRP 120

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us-10-067-482-2.rag

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QY 121 NSGDEKRLSLSEGKVKXNMGKXRVSSGSSRGSKSPKRAQEQSPKRGPPPKDEKD 180
Db 121 NSGDEKRLSLSEGKVKXNMGKXRVSSGSSRGSKSPKRAQEQSPKRGPPPKDEKD 180
QY 181 LIPESSTVKGMMAGPMAFKWQPTASEPVKQADPHFHFLLSQTEKPAVCYQAIKKLK 240
Db 181 LIPESSTVKGMMAGPMAFKWQPTASEPVKQADPHFHFLLSQTEKPAVCYQAIKKLK 240
QY 241 ICEE 244
Db 241 ICED 244

RESULT 12
AAU20553
ID AAU20553 standard; protein; 260 AA.
XX
AC AAU20553;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human secreted protein, Seq ID No 545.
XX
KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
KW rheumatoid arthritis; antiarteriosclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
KW cytotatic; Alzheimer's disease; Parkinson's disease; human; cancer;
KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
KW Gaucher's disease; neurological disease; cerebrovascular disorder;
KW thrombosis; wound healing.
XX
OS Homo sapiens.
XX
PN W0200155326-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001347.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
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PR 08-NOV-2000; 2000US-0246478P.
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PR 17-NOV-2000; 2000US-0249297P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465558/50.
XX N-PSDB; AAS34946.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
XX diagnose diseases or disorders associated with aberrant expression or
XX activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
XX Claim 11; SEQ ID NO 474; 687pp; English.
XX
XX The present invention relates to the isolation of novel human neoplastic
XX disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA
XX sequences encoding for these polypeptides. The sequences of the invention
XX are useful in the diagnosis, treatment, prevention and/or prognosis of
XX disorders involving neoplastic disease such as hyperproliferative
XX disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
XX glioma, adult liver cancer, childhood cerebellar astrocytoma, or
XX Hodgkin's lymphoma). The sequences of the invention may also be useful
XX for treating other disorders such as neural disorders, immune system
XX disorders, muscular disorders, reproductive disorders, gastrointestinal
XX disorders, pulmonary disorders, cardiovascular disorders and renal
XX disorders. The polynucleotide sequences of the invention are also useful
XX in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
XX disease associated polypeptides of the invention. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 260 AA;
XX
XX Query Match 45.0%; Score 1291; DB 4; Length 260;
XX Best Local Similarity 99.6%; Pred. No. 3.2e-110;

Matches	243;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MAAVSLRLGDLVWGKLGRLGYPWPVKI	VPKPPKDLKKPRGKCKFFVKFFGTE	HAMIKV	EQ	60			
Db	12	MAAVSLRLGDLVWGKLGRLGYPWPVKI	VPKPPKDLKKPRGKCKFFVKFFGTE	HAMIKV	EQ	71			
Qy	61	KPYHAKEEMIKKNGKRFQAVDAVEFL	PRAKGDKQTSSHNSDDKNNRNSSEERS	SRP	120				
Db	72	KPYHAKEEMIKKNGKRFQAVDAVEFL	PRAKGDKQTSSHNSDDKNNRNSSEERS	SRP	131				
Qy	121	NSGDEKRLSLSEGVKKNMGEGKRYSS	SGSRGSKPLKRAQEOSPRKGRPPK	DEK	180				
Db	132	NSGDEKRLSLSEGVKKNMGEGKRYSS	SGSRGSKPLKRAQEOSPRKGRPPK	DEK	191				
Qy	181	LTIPESSTVGMWAGPMAAFKMQPTASE	PKVADDPHFHFLLSQTEKPAVCYQAI	TKLK	240				
Db	192	LTIPESSTVGMWAGPMAAFKMQPTASE	PKVADDPHFHFLLSQTEKPAVCYQAI	TKLK	251				
Qy	241	ICEE	244						
Db	252	ICED	255						

RESULT 14

ADC46388
ID ADC46388 standard; protein; 260 AA.

AC ADC46388;

XX
DT 18-DEC-2003 (first entry)

XX
DE Human neoplastic disease-associated gene 23 protein #2.

XX
KW Neoplastic disease-associated polypeptide; gene therapy;
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; Crohn's disease; neurodegenerative disorder;
KW inflammatory bowel disease; Parkinson's disease; renal disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human.

XX
OS Homo sapiens.

XX
PN US2003082758-A1.

XX
XX 01-MAY-2003.

XX
PF 22-MAR-2002; 2002US-00103313.

XX
XX 31-JAN-2000; 2000US-0179065P.

XX
PR 04-FEB-2000; 2000US-0180628P.

XX
PR 24-FEB-2000; 2000US-0184664P.

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PR 18-APR-2000; 2000US-0198123P.

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PR 30-JUN-2000; 2000US-0214886P.

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PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0253678P.
PR 17-JAN-2001; 2001US-00764854.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-786918/74.
XX N-PSDB; ADC46104.
XX New isolated human neoplastic disease-associated polypeptides and
XX polynucleotides, useful for diagnosing, preventing, prognosticating or
XX treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
XX disease.
XX Claim 11; SEQ ID NO 474; 302pp; English.
XX The invention relates to one of 238 disclosed human neoplastic disease-
XX associated polypeptides encoded by 171 disclosed cDNA sequences
XX (including their domains, epitopes, full-length proteins, allelic variants
XX or species homologues). Also included are there encoding nucleic acids, a
XX recombinant vector comprising the nucleic acid, a recombinant host cell
XX comprising the nucleic acid (expressing the protein), an isolated
XX antibody that binds specifically to the isolated polypeptide, preventing,
XX treating or ameliorating a medical condition, diagnosing a pathological
XX condition or a susceptibility to a pathological condition in a subject,
XX identifying a binding partner to the polypeptide, identifying an activity
XX in a biological assay, and the gene corresponding to the cDNA sequence.
XX The polypeptides, polynucleotides and antibodies are useful for
XX detecting, preventing, diagnosing, prognosticating, treating or

CC ameliorating medical conditions such as hyperproliferative diseases or
CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC anaemia or thrombocytopaenia), allergic reactions including asthma or
CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
Query Match 45.0%; Score 1291; DB 7; Length 260;
Best Local Similarity 99.6%; Pred. No. 3.2e-110;
Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVSLRLGDLVWGKLGKGRYPVPPGKIYNPKDLKKRGGKCFVKGFGTGDHAWIKVEQL 60
DB 12 MAAVSLRLGDLVWGKLGKGRYPVPPGKIYNPKDLKKRGGKCFVKGFGTGDHAWIKVEQL 71
QY 61 KPYHAHKEEMIKKNGKRFQAVDAVEEFLRRAGKQDTSSHNSSDDKNRNSSEERSRP 120
DB 72 KPYHAHKEEMIKKNGKRFQAVDAVEEFLRRAGKQDTSSHNSSDDKNRNSSEERSRP 131
QY 121 NSGDEKRLSLSEGVKKNMGEGKRVSSGSSRGSKSPDKRAQEQSPKRGRRPKDEKD 180
DB 132 NSGDEKRLSLSEGVKKNMGEGKRVSSGSSRGSKSPDKRAQEQSPKRGRRPKDEKD 191
QY 181 LTTPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITKKLK 240
DB 192 LTTPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITKKLK 251
QY 241 ICBE 244
DB 252 ICED 255
RESULT 15
AAU21590
ID AAU21590 standard; protein; 250 AA.
XX AC AAU21590;
XX DT 04-DEC-2001 (first entry)
XX XX Novel human neoplastic disease associated polypeptide #23.
XX Human; neoplastic disease associated polypeptide; cancer;
XX hyperproliferative disorder; neural disorder; immune system disorder;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX neuroprotective; cytostatic; anti inflammatory; vasotropic.
XX OS Homo sapiens.
XX WO200155163-A1.
XX PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US0001358.
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
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 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-465558/50.
 N-PSDB; AAS34789.
 Novel polypeptides and polynucleotides useful as diagnostic reagents to
 diagnose diseases or disorders associated with aberrant expression or
 activity of polypeptides, and for treating cancers, rheumatoid arthritis.
 Claim 11; SEQ ID NO 317; 687pp; English.
 The present invention relates to the isolation of novel human neoplastic
 disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA
 sequences encoding for these polypeptides. The sequences of the invention
 are useful in the diagnosis, treatment, prevention and/or prognosis of
 disorders involving neoplastic disease such as hyperproliferative
 disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
 glioma, adult liver cancer, childhood cerebellar astrocytoma, or
 Hodgkin's lymphoma). The sequences of the invention may also be useful
 for treating other disorders such as neural disorders, immune system
 disorders, muscular disorders, reproductive disorders, gastrointestinal
 disorders, pulmonary disorders, cardiovascular disorders and renal
 disorders. The polynucleotide sequences of the invention are also useful
 in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic

Thu Sep 16 09:36:51 2004

us-10-067-482-2.rag

CC disease associated polypeptides of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 250 AA;

Query Match	44.9%	Score 1286;	DB 4;	Length 250;
Best Local Similarity	99.6%	Pred. No. 8.7e-110;		
Matches 242;	Conservative	1;	Mismatches 0;	Indels 0; Gaps 0;

QY	2	AAVSLRLGDLVWVGKLGKRYPPWPKGKIVNPPKDLKKPRGKKCFVVKFFGTEDHAMIKVEQLK	61
Db	3	AAVSLRLGDLVWVGKLGKRYPPWPKGKIVNPPKDLKKPRGKKCFVVKFFGTEDHAMIKVEQLK	62
QY	62	PYHAHKEEMIKINKGKRFQOAVDAVEEFLRAKGDQTSNHSDDDKRRNSSEERSRPN	121
Db	63	PYHAHKEEMIKINKGKRFQOAVDAVEEFLRAKGDQTSNHSDDDKRRNSSEERSRPN	122
QY	122	SGDEKRLSLSEGVKKNMGEGKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKDL	181
Db	123	SGDEKRLSLSEGVKKNMGEGKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKDL	182
QY	182	TIPESSTVKGMMAGPMAFKWQPTASEPVKDADPHFHHLLSOTKPAVCYQAITKKIKI	241
Db	183	TIPESSTVKGMMAGPMAFKWQPTASEPVKDADPHFHHLLSOTKPAVCYQAITKKIKI	242
QY	242	CEE 244	
Db	243	CED 245	

RESULT 16
ADC46231
ID ADC46231 standard; protein; 250 AA.

XX AC ADC46231;

XX DT 18-DEC-2003 (first entry)

XX DE Human neoplastic disease-associated gene 23 protein #1.

XX Neoplastic disease-associated polypeptide; gene therapy;
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human.

XX OS Homo sapiens.

XX PN US2003082758-A1.

XX PD 01-MAY-2003.

XX PF 22-MAR-2002; 2002US-00103313.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189374P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.

20-OCT-2000; 2000US-0241787P.
 20-OCT-2000; 2000US-0241808P.
 20-OCT-2000; 2000US-0241809P.
 01-NOV-2000; 2000US-0241826P.
 08-NOV-2000; 2000US-0244617P.
 08-NOV-2000; 2000US-0246474P.
 08-NOV-2000; 2000US-0246475P.
 08-NOV-2000; 2000US-0246476P.
 08-NOV-2000; 2000US-0246477P.
 08-NOV-2000; 2000US-0246478P.
 08-NOV-2000; 2000US-0246523P.
 08-NOV-2000; 2000US-0246524P.
 08-NOV-2000; 2000US-0246525P.
 08-NOV-2000; 2000US-0246526P.
 08-NOV-2000; 2000US-0246527P.
 08-NOV-2000; 2000US-0246528P.
 08-NOV-2000; 2000US-0246532P.
 08-NOV-2000; 2000US-0246609P.
 08-NOV-2000; 2000US-0246610P.
 08-NOV-2000; 2000US-0246611P.
 17-NOV-2000; 2000US-0246613P.
 17-NOV-2000; 2000US-0249207P.
 17-NOV-2000; 2000US-0249208P.
 17-NOV-2000; 2000US-0249209P.
 17-NOV-2000; 2000US-0249210P.
 17-NOV-2000; 2000US-0249211P.
 17-NOV-2000; 2000US-0249212P.
 17-NOV-2000; 2000US-0249213P.
 17-NOV-2000; 2000US-0249214P.
 17-NOV-2000; 2000US-0249215P.
 17-NOV-2000; 2000US-0249216P.
 17-NOV-2000; 2000US-0249217P.
 17-NOV-2000; 2000US-0249218P.
 17-NOV-2000; 2000US-0249244P.
 17-NOV-2000; 2000US-0249245P.
 17-NOV-2000; 2000US-0249264P.
 17-NOV-2000; 2000US-0249265P.
 17-NOV-2000; 2000US-0249297P.
 17-NOV-2000; 2000US-0249299P.
 01-DEC-2000; 2000US-0249300P.
 01-DEC-2000; 2000US-0250160P.
 05-DEC-2000; 2000US-0250391P.
 05-DEC-2000; 2000US-0251030P.
 05-DEC-2000; 2000US-0251988P.
 06-DEC-2000; 2000US-0256719P.
 08-DEC-2000; 2000US-0251479P.
 08-DEC-2000; 2000US-0251856P.
 08-DEC-2000; 2000US-0251868P.
 08-DEC-2000; 2000US-0251869P.
 08-DEC-2000; 2000US-0251989P.
 11-DEC-2000; 2000US-0251990P.
 05-JAN-2001; 2000US-0254097P.
 17-JAN-2001; 2001US-0259678P.
 17-JAN-2001; 2001US-00764854.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM, Barash SC;
 WPI; 2003-786918/74.
 N-PSDB; ADC45947.
 New isolated human neoplastic disease-associated polypeptides and polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's disease.
 Claim 11; SEQ ID NO 317; 302pp; English.
 The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variants or species homologues). Also included are there encoding nucleic acids, a

recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the polypeptide, identifying an activity in a biological assay, and the gene corresponding to the cDNA sequence. The polypeptides, polynucleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematologic disorders (e.g. anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury, Query Match 44.9%; Score 1286; DB 7; Length 250; Best Local Similarity 99.6%; Pred. No. 8.7e-110; Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVSLRLGLVWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKFGTDEHAWIKVQLK 61
 DB 3 AAVSLRLGLVWGKLGKRYPPWPKIVNPPKDLKKPRGKCKFFVKFGTDEHAWIKVQLK 62
 QY 62 PYHAHKEEMIKINKKRFQQAQVDAVEFLRRAKCKDQTSNHSDDDKNRRNSSEERSPN 121
 DB 63 PYHAHKEEMIKINKKRFQQAQVDAVEFLRRAKCKDQTSNHSDDDKNRRNSSEERSPN 122
 QY 122 SGDEKRLKLSLGKVKKNMGEGKRYSSGSSRGSKSPLKRAQEQSPKRGPRPKDKDL 181
 DB 123 SGDEKRLKLSLGKVKKNMGEGKRYSSGSSRGSKSPLKRAQEQSPKRGPRPKDKDL 182
 QY 182 TIPSSTVKGMMAGPMAAFKMQPTASEPVKADPHFHHLLSQTEKPAVCYQAITKKLI 241
 DB 183 TIPSSTVKGMMAGPMAAFKMQPTASEPVKADPHFHHLLSQTEKPAVCYQAITKKLI 242
 QY 242 CEE 244
 DB 243 CED 245

RESULT 17
 ABB60930
 ID ABB60930 standard; protein; 574 AA.
 AC ABB60930;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 9582.
 DE Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US009231.
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL05033.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 9582; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 574 AA;

Query Match 26.8%; Score 769.5; DB 4; Length 574;
Best Local Similarity 32.6%; Pred. No. 1.5e-61;
Matches 188; Conservative 108; Mismatches 22; Indels 59; Gaps 13;
QY 19 YPPWPGKIVNPPKDL---KKPRGKKCFVKFFGTEHAWIKVEQLKPYHA-HKEEMIKIN 74
DB 5 FTFWPGMIVDPLDLLSOQRANTKCVF--PFGSRNFAWIEENNIKPEGPWKEELAKVS 62
QY 75 KGKRFQQAADVAEFLRAKQKDOTSHNSDDKNNRNSSESRPNRSGDEKRKLISSEG 134
DB 63 KPAAFRAHMTDIEKYIDDPAEVDEQVKNKSCGAPNHATEADFDKIR--DGLDSEISVGEA 120
QY 135 KVKKMGKGRVSGSSERG-----SKSL-----KRAEQSQSPR----- 169
DB 121 TADGNGGVVAHV--GSPDEGDGLVEINADSSAPVTSVPAVTTKAGKRTPKAKSVAA 178
QY 170 ---KRGPRPKDEKDLTTPESSTVKGMAGMAAFKMQPTAS-BPVKDADP----- 215
DB 179 SVKSTGSAKSAQKRTSAQOSP-----SGPSNAKRGKRDVSGEALQADAEASSTPTGRR 233
QY 216 --HFHFHLLSQTEKPAVCYQAITKKLICEBTGTSTQADSTAVNGSIPTDKIGFL 273
DB 234 RVETDALLASTAAKRAPNAIALLDPRVTRPEAQVIDMSRSNTLADRDIVPSEQTFGL 293
QY 274 GLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVYSTCDITPAVCSD 333
DB 294 GLGMMGSTIVKDLITVGHKVVVNNITDKQCPFAAGAEVKDTPMDVVEADVIECCVSD 353
QY 334 PKAAKDLVLGPGSVLQGIKP--GKCYVDMSTVDADTVTELAQVIVSRGRFLFPAVSGNQ 391
DB 354 PKGAKDLVFGNGCVLQ-LKDLNKAAYVENSTIDPDTSLDIGIKQCNRYLEAQIHGSR 412
QY 392 QLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIIVNMVQSGPMATI 451
DB 413 QEAEEGMLIILAGGDSRVFECHSCFKTKAKNTFFLGNIGNACKKNLILQTLIGSLVGL 472
QY 452 AEGTLIAHVTVGSOQQLLDILNOGQLASIFLDQKQCNILQGNFKPDPFYLKYIKQDLRLAI 511
DB 473 AEALALADRFSLNDIIDIIFDLSWKSPMLLAKGEMAKGDFNFPQPLSHNQDRLRLVL 532
QY 512 ALGDVAVNHTPMAAAANEVYKRAKALDQSDNDMSAVY 548
DB 533 NNAENLDQSNPVTISITNEVFHKTKRLGYSEHDSAVF 569

RESULT 18
AAE19927
ID AAE19927 standard; protein; 360 AA.
XX
AC AAE19927;
XX
DT 18-JUN-2002 (first entry)
XX
DE Corn 3-hydroxyisobutyrate dehydrogenase #2.
XX

KW Branched chain amino acid degradation enzyme; HMG-CoA lyase;
KW 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
KW isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31.
XX
OS Zea mays.
XX
PN US6348339-B1.
XX
PD 19-FEB-2002.
XX
PF 29-JUL-1999; 99US-00364230.
XX
PR 31-JUL-1998; 98US-0094990P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;
XX
DR WPI; 2002-204621/26.
DR N-PSDB; AAD31748.
XX
PT Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used
PT to produce transgenic plants having an altered expression of the enzyme.
XX
PS Claim 1; Col 27-30; 40pp; English.
XX
CC The invention relates to nucleic acid fragments encoding branched chain
CC amino acid degradation enzymes. Particularly the invention relates to 3-
CC hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA)
CC lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides
CC derived from corn, rice and wheat. Sequences of the invention are used to
CC produce transgenic plants having an altered expression of the enzyme.
CC Polynucleotides of the invention can be used as probes for physical
CC mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate
CC dehydrogenase (EC 1.1.1.31) from crln.pk0191.b10, p0076.cwhan08r and
CC p0118.chsbe01r clones
XX
SQ Sequence 360 AA;
Query Match 25.6%; Score 733; DB 5; Length 360;
Best Local Similarity 52.3%; Pred. No. 1.6e-58;
Matches 148; Conservative 47; Mismatches 88; Indels 0; Gaps 0;
QY 266 TDKTIGTGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVYSTCD 325
DB 64 SEMEVGLGIGMGKAMATNLLRHGFRVTVNRTLAKQELAAALGATVGETPASVVKCR 123
QY 326 ITFACVSPKAAKDLVLGPGSVLQGIKPGKCYVDMSTVDADTVTELAQVIVSRGRFLFLEA 385
DB 124 YTIAMLSDFSAAALSVPFDKGVLEIQIGSGKGVDMSTVDADTATSTKISEAVKQGGAFLEA 183
QY 386 PVSNGMOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIIVNMVQ 445
DB 184 PVSNGKKAEDQQLVILAAGDKPLVDGMPAFDVLGKKSFFLGEVGNAAKMMLIIVNMVQ 243
QY 446 SPMTAIEGLTIAHVTVGSOQQLLDILNOGQLASIFLDQKQCNILQGNFKPDPFYLKYIK 505
DB 244 SMWNSLSEGLCLADKSGLSQPLLDVLDLGAITNPMFKLKGPTMDGSSYPAPFLKHQOK 303
QY 506 DLRLAIALGDVAVNHTPMAAAANEVYKRAKALDQSDNDMSAVY 548
DB 304 DMRLALALGDENAVAMPVSAANAANFAKARSILGLGDQDFSAVY 346
RESULT 19
AAE36391
ID AAE36391 standard; protein; 290 AA.
XX
AC AAE36391;
XX
DT 26-JUN-2003 (first entry)
XX
DE Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue.

Db 242 LALALGDNANVNFVAAAANAEAFKARSGLGLDLSFSAVIEA 283

RESULT 21

AAEL19929 ID AAE19929 standard; protein; 345 AA.

XX AC AAE19929;

DT 18-JUN-2002 (first entry)

XX Soybean 3-hydroxyisobutyrate dehydrogenase #1.

XX Branched chain amino acid degradation enzyme; HMG-CoA lyase;
KW 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
KW isovaleryl-CoA dehydrogenase; transgenic plant; soybean; EC 1.1.1.31.

XX Glycine max.

XX US6348339-B1.

XX 19-FEB-2002.

XX 29-JUL-1999; 99US-00364230.

XX 31-JUL-1998; 98US-0094990P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;

XX WPI; 2002-204621/26.

XX N-PSDB; RAD31750.

XX Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used
PT to produce transgenic plants having an altered expression of the enzyme.

XX Claim 1; Col 33-36; 40pp; English.

XX The invention relates to nucleic acid fragments encoding branched chain
XX amino acid degradation enzymes. Particularly the invention relates to 3-
XX hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA)
XX lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides
XX derived from corn, rice and wheat. Sequences of the invention are used to
XX produce transgenic plants having an altered expression of the enzyme.
XX Polynucleotides of the invention can be used as probes for physical
XX mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate
XX dehydrogenase (EC 1.1.1.31) from ses2w.pk0002.e5 clone

XX Sequence 345 AA;

Query Match 23.8%; Score 682; DB 5; Length 345;

Best Local Similarity 47.1%; Pred. No. 7.7e-54;

Matches 136; Conservative 54; Mismatches 99; Indels 0; Gaps 0;

QY 262 SITPTDKKIGFLGLMGSGIVSNLLKMGHTVTVMNRATKCDLFTQEGARLGRTPAEV 321

DB 46 AVTEPPARIGFLGLMGSPMAHNLKAGVDLTVMNRATKCDLFTQEGARLGRTPAEV 105

QY 322 STCDLTFACVSPKAAKDLVLGPGSVLQIRPKCYVDMSTVDADTVTELAVIVSRGR 381

DB 106 ASCDVTFAMLADPQSNADVACGKHGAANGPGKGVVDVSTVGDTSKLINGHMRKSTGAL 165

QY 382 FLEAPVSGNQQLSNDGMLVILAGDRGLYEDSCSCFQAMGKTSFFLGEVGNAAKMLIVN 441

DB 166 FLEAPVSGSKPAEDQLIFLTAGDKNLYEAVGSLDDINGKSKFYLDGVNGAAMKLVN 225

QY 442 MVQSGFWATIAEGLTLAHVTGQSQQTLDDILNQGQLASIFLDQKCNILQGNFKPDPFLK 501

DB 226 MINGSMWAGFSEGLLSEKVGLDPPVILVQVWSGALISAPMYSTKGFMSIQSLYPTAFPLK 285

QY 502 YIQKDLRLALGLAELGLAESVSQPTPIASAANELYKVAKNSGLSDQDFSAVIEA 550

Db 286 HQOKDLRLALGLAELGLAESVSQPTPIASAANELYKVAKNSGLSDQDFSAVIEA 334

RESULT 22

AAE19491

ID AAE19491 standard; protein; 289 AA.

XX AC AAE19491;

DT 06-MAR-2001 (first entry)

XX Amino acid sequence of gamma-hydroxy butyrate dehydrogenase (GHBHDH).

XX Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
KW gamma-hydroxy butyrate dehydrogenase; GHBHDH; succinic semialdehyde;
KW gamma hydroxybutyrate.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

XX Misc-difference 1..100

XX /note= "these residues are encoded by nucleotides 1-300"

XX WO200061763-A2.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-CA000378.

XX 09-APR-1999; 99US-0128518P.

XX (UYGU-) UNIV GUELPH.

XX Shelp BJ, Breitzkreuz KE, Van Cauwenberghe OR;

XX WPI; 2000-679492/66.

XX N-PSDB; AAC62027.

XX Novel proteins related to gamma aminobutyric acid (GABA) metabolism, GABA
XX -transaminase and gamma hydroxy butyrate dehydrogenase useful for
XX screening and isolation of homologous genes from other organisms.

XX Claim 18; Fig 5; 48pp; English.

XX The present sequence represents a plant gamma-hydroxy butyrate
XX dehydrogenase (GHBHDH). The specification also describes a plant gamma-
XX aminobutyric acid (GABA) transaminase (GABA-T). The proteins are involved
XX in the metabolism of GABA in plants. GABA-T is used to transaminase GABA
XX to form succinic semialdehyde, which may be converted to gamma
XX hydroxybutyrate by GHBHDH. The polynucleotides are used to produce GABA-T
XX and GHBHDH recombinantly. The proteins are useful for screening and
XX isolation of homologous genes from other organisms

XX Sequence 289 AA;

Query Match 23.7%; Score 679; DB 3; Length 289;

Best Local Similarity 48.6%; Pred. No. 1.1e-53;

Matches 137; Conservative 49; Mismatches 96; Indels 0; Gaps 0;

QY 269 KTGFLGLMGSGIVSNLLKMGHTVTVMNRATKCDLFTQEGARLGRTPAEVSTCDITF 328

DB 2 EYGFGLGIMGKAMGNLLKNGFKVTVMNRATLTKCDLVEHGASVCESPAEVIKKCKYTI 61

QY 329 ACVSDPKAAKDLVLGPGSVLQIRPKCYVDMSTVDADTVTELAVIVSRGRFLAPVS 388

DB 62 AMLSDFCAALSVDKGGVLEQICEKGVIDMSTVDAETSLKINEAITGKGRFVGPVS 121

QY 389 GNOQSLNDCMLVILAGDRGLYEDSCSCFQAMGKTSFFLGEVGNAAKMLIVNMVQSGFM 448

DB 122 GSKKPAEDQLIFLTAGDKNLYEAVGSLDDINGKSKFYLDGVNGAAMKLVNMGSM 181

QY 449 ATTAEGTLIAHVTGQSQQTLDDILNQGQLASIFLDQKCNILQGNFKPDPFLKYIQKDLR 508

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PR	16-AUG-1999;	99US-0149368P.	Db	92	RTSKCDPLVLGAKYKSSPEEVTACDLTFAMLADESAIDVACGKNGAIFGISSGKY	151
PR	17-AUG-1999;	99US-0149426P.	Qy	358	VDMSVTVDADTVELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSCCF	417
PR	18-AUG-1999;	99US-0149722P.	Db	152	VDVSTVDVASSILLISKQIKOTGALFLEAPVSGSKKPAEDGQLIFLTAGDKFELYEKAAPFL	211
PR	20-AUG-1999;	99US-0149723P.	Qy	418	QAMGKTSFFLGEVGNAAKMMLIYNNVOGSEFWATTAEGTLTAHVTVGQSQOQLDILNOSQL	477
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PR	25-AUG-1999;	99US-0150566P.	Db	272	NAPMYSLKGFSPMIKSVVYPTAFPLKHQOKDMELALGLAESVSQSTPIAAAANELYKVAKY	331
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Qy	238	KLKICEETGTSIQADSTAVNGSIPTDKKIGFLGLGIMGSGIVSNLLKMGHTVTVMN	297			

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DB 121 EDGQLIFLTAGDKPLYEKAAPFLDIMGSKFYLGVEGNGAAMKLVNWMINGSWWSFAEG 180

QY 455 LTLAHTVGSQOQTLILLINQOQLASIFLDOKCONIQGNFKPDFYLYIKQDLRLAIALG 514
DB 181 ILLSKQVGLDPNVLVFWVWSQAINAPMYSILKGPSMKSVYPTAFPLKHQOKDMRLAIGLA 240

QY 515 DAVNHPTMAAAANVYKRAKALDQSDNDMSAVYRA 550
DB 241 ESVSQSTPIAAANVYKRAKALDQSDNDFSAVIEA 276

RESULT 26
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AC AAE19926;
XX
DT 18-JUN-2002 (first entry)
XX
DE Corn 3-hydroxyisobutyrate dehydrogenase #1.
XX
KW Branched chain amino acid degradation enzyme; HMG-CoA lyase;
KW 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
KW isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT Misc-difference 244 /label= Unknown
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FT Misc-difference 247 /label= Unknown
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XX
PN US6348339-B1.
XX
PD 19-FEB-2002.

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XX 29-JUL-1999; 99US-00364230.
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XX 31-JUL-1998; 98US-0094990P.
XX PR
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XX PA
XX Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;
XX WPI; 2002-204621/26.
XX PI
XX N-PSDB; AAD31747.
XX DR
XX Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used
XX PT to produce transgenic plants having an altered expression of the enzyme.
XX PS
XX Disclosure; Col 23-26; 40pp; English.
XX XX
XX The invention relates to nucleic acid fragments encoding branched chain
XX CC amino acid degradation enzymes. Particularly the invention relates to 3-
XX CC hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA)
XX CC lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides
XX CC derived from corn, rice and wheat. Sequences of the invention are used to
XX CC produce transgenic plants having an altered expression of the enzyme.
XX CC Polynucleotides of the invention can be used as probes for physical
XX CC mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate
XX CC dehydrogenase (EC 1.1.1.31) from cemin.pk0138.e1, ctain.pk0052.d10 and
XX CC p0037.crwak74r clones
XX XX
XX Sequence 247 AA;
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XX Query Match 18.8%; Score 537.5; DB 5; Length 247;
XX Best Local Similarity 45.3%; Pred. No. 9.8e-41;
XX Matches 106; Conservative 47; Mismatches 80; Indels 1; Gaps 1;
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Qy 284 SNLLKMGHTVTVNRTAKCDLFTOEGARLGRTPAEVVSTCDITPACVSDPKAAKDLVLG 343
Db 2 SNLIAGCDVTVNRTKSCDPLSLGAKYEPTPAQVASSCDVTFAMLADPQSAAEVACG 61
Qy 344 PSGLVQIRPKCVYDMSTVDADTVTELAQVIVSRGGRFLAPVSGNQOLNDGMLVILA 403
Db 62 SSGAAEGLAPGKYVDVSTVDGATSKLIGERTITSGASFLEAPVSGSKKPAEDGLILFT 121
Qy 404 AGDRGLYEDSCSCFQMGKTSFFELGCVGNAAKMWLVNVOGSEFMATIAEGLTLAHVTGQ 463
Db 122 AGDESLYKRVAPLDDVMGKSRFYLGDVGNAAKLVNVMGSMVVSFSEGLLLSEKVLG 181
Qy 464 SQOTLLDILNOGLASIFLDQKCONILOGNFPKDFYLYIQKDLRLAIALGDVAV 517
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QY	314	GRTPAEVWSTCDITFACYSDDPKAAKDVLGP-SGVLOGLRPGKCVVDMSTVDADTVTELA 372
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QY	373	QVIVSRGGRFLEAPVSGNQQLSNDQMLVILAAGRLYEDCSSCFQAMGKTSFFLGEVGN 432
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QY	433	AAKMMLIVNVOGSPMATIAGLTIAHVTGQSQQTLLDILNOGQLASFLDQKCCNIIQQ 492
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QY 373 QVIVSRGGRFLRPSGNGQNSDGMVLTLAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
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Search completed: September 16, 2004, 07:30:35
Job time : 69 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:28:53 ; Search time 19 seconds
(without alignments)
1502.587 Million cell updates/sec

Title: **US-10-067-482-2**

Perfect score: 2866

Sequence: 1 MAAVSLRLGLVWKLGRYP.....AKALDQSDNDSAVYRIYH 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : **Issued Patents AA:***

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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
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4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
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6: /cgn2_6/prodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	733	25.6	360	4	US-09-364-230-4
3	682	23.8	345	4	US-09-364-230-8
4	537.5	18.8	247	4	US-09-364-230-2
5	364	12.7	307	4	US-09-489-039A-9294
6	343.5	12.0	299	4	US-09-328-352-7407
7	343	12.0	543	4	US-09-252-991A-27650
8	340	11.9	299	4	US-09-107-532A-5109
9	326	11.4	304	4	US-09-489-039A-9424
10	324.5	11.3	324	4	US-09-252-991A-26001
11	310	10.8	330	4	US-09-252-991A-17923
12	301.5	10.5	292	4	US-09-711-164-438
13	291	10.2	295	4	US-09-252-991A-24727
14	287.5	10.0	303	4	US-09-328-352-4879
15	266	9.3	326	4	US-09-328-352-4879
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17	252	8.8	247	4	US-09-134-000C-5460
18	240.5	8.4	350	4	US-09-364-230-12
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21	208	7.3	221	4	US-09-252-991A-22003
22	185.5	6.5	237	2	US-08-760-745-5
23	185.5	6.5	240	2	US-08-760-745-3
24	178.5	6.2	235	2	US-08-760-745-1
25	161.5	5.6	234	4	US-09-364-230-10
26	148.5	5.2	1360	4	US-09-788-657-22
27	145	5.1	490	4	US-09-489-039A-8350

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29	138.5	4.8	316	4	US-09-252-991A-29147	Sequence 29147, A
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32	135.5	4.7	787	3	US-09-312-283C-334	Sequence 334, App
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36	121.5	4.2	1024	4	US-09-562-737-49	Sequence 49, Appl
37	120	4.2	949	4	US-10-164-595-65	Sequence 65, Appl
38	120	4.2	1214	4	US-10-164-595-24	Sequence 24, Appl
39	118.5	4.1	1312	4	US-09-134-001C-3241	Sequence 29, Appl
40	118	4.1	474	4	US-09-134-001C-3241	Sequence 3241, Ap
41	117	4.1	723	4	US-09-252-991A-29659	Sequence 29659, A
42	113.5	4.0	289	4	US-09-107-532A-7169	Sequence 7169, Ap
43	112.5	3.9	909	3	US-09-425-383-2	Sequence 2, Appli
44	112	3.9	1005	4	US-09-206-942-41	Sequence 41, Appl
45	112	3.9	1011	4	US-09-206-942-39	Sequence 39, Appl
46	111.5	3.9	720	4	US-09-252-991A-18618	Sequence 18618, A
47	111	3.9	562	2	US-08-973-675-2	Sequence 2, Appli
48	111	3.9	605	4	US-08-714-741-46	Sequence 46, Appl
49	111	3.9	1187	1	US-08-320-559-28	Sequence 28, Appl
50	111	3.9	1187	3	US-08-545-860D-28	Sequence 28, Appl
51	111	3.9	1187	5	PCT-US94-04496-28	Sequence 28, Appl
52	111	3.9	1210	1	US-08-320-559-26	Sequence 26, Appl
53	111	3.9	1210	3	US-08-545-860D-26	Sequence 26, Appl
54	111	3.9	1210	5	PCT-US94-04496-26	Sequence 26, Appl
55	110.5	3.9	598	3	US-09-377-155-5	Sequence 5, Appli
56	110.5	3.9	598	3	US-09-377-155-13	Sequence 13, Appl
57	110.5	3.9	598	4	US-09-669-974-5	Sequence 5, Appli
58	110.5	3.9	598	4	US-09-669-974-13	Sequence 13, Appl
59	110.5	3.9	598	4	US-09-797-862-5	Sequence 5, Appli
60	110.5	3.9	598	4	US-09-797-862-13	Sequence 13, Appl
61	110.5	3.9	1581	3	US-09-110-517-2	Sequence 2, Appli
62	110	3.8	1007	4	US-09-489-039A-11327	Sequence 11327, A
63	109.5	3.8	1964	2	US-08-790-912-3	Sequence 3, Appli
64	109.5	3.8	2052	2	US-08-790-912-3	Sequence 2, Appli
65	108	3.8	909	2	US-08-363-124A-4	Sequence 4, Appli
66	108	3.8	2184	4	US-09-417-485D-6	Sequence 6, Appli
67	107.5	3.8	699	4	US-09-759-359A-2	Sequence 2, Appli
68	107	3.7	585	4	US-09-134-000C-3802	Sequence 3802, Ap
69	106.5	3.7	320	4	US-09-134-000C-5021	Sequence 5021, Ap
70	106	3.7	2860	2	US-08-826-267-2	Sequence 2, Appli
71	105.5	3.7	334	4	US-09-198-452A-923	Sequence 2, Appli
72	105.5	3.7	688	2	US-09-016-000-2	Sequence 2, Appli
73	104.5	3.6	365	2	US-08-515-251A-2	Sequence 2, Appli
74	104.5	3.6	688	3	US-09-141-047-8	Sequence 8, Appli
75	104.5	3.6	921	4	US-09-543-681A-5734	Sequence 5734, Ap
76	104.5	3.6	2468	4	US-09-976-594-726	Sequence 726, App
77	104	3.6	754	4	US-09-976-594-375	Sequence 375, App
78	103.5	3.6	568	1	US-08-320-559-30	Sequence 30, Appl
79	103.5	3.6	568	5	PCT-US94-04496-30	Sequence 30, Appl
80	103.5	3.6	568	5	PCT-US94-04496-30	Sequence 30, Appl
81	103	3.6	204	4	US-09-198-452A-376	Sequence 376, App
82	103	3.6	277	4	US-09-489-039A-12994	Sequence 12994, A
83	102.5	3.6	594	3	US-09-377-155-7	Sequence 7, Appli
84	102.5	3.6	594	4	US-09-669-974-7	Sequence 7, Appli
85	102.5	3.6	594	4	US-09-797-862-7	Sequence 7, Appli
86	102	3.6	722	4	US-09-392-714-22	Sequence 22, Appl
87	102	3.6	912	4	US-09-540-236-1960	Sequence 1960, Ap
88	101.5	3.5	930	3	US-09-283-763-2	Sequence 2, Appli
89	101.5	3.5	930	4	US-09-574-912-2	Sequence 2, Appli
90	101.5	3.5	947	4	US-09-418-780A-1	Sequence 1, Appli
91	101.5	3.5	947	4	US-09-392-714-23	Sequence 23, Appl
92	101.5	3.5	3025	6	5223423-3	Patent No. 5223423
93	101	3.5	751	4	US-09-252-991A-27424	Sequence 27424, A
94	101	3.5	1835	3	US-08-836-325-15	Sequence 15, Appl
95	100.5	3.5	433	4	US-08-630-915A-18	Sequence 18, Appl
96	100.5	3.5	592	3	US-09-377-155-17	Sequence 17, Appl
97	100.5	3.5	592	4	US-09-669-974-17	Sequence 17, Appl
98	100.5	3.5	592	4	US-09-797-862-17	Sequence 17, Appl
99	100.5	3.5	733	3	US-08-725-459B-21	Sequence 21, Appl
100	100.5	3.5	1024	4	US-09-562-737-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-10-164-595-72

Sequence 72, Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:

APPLICANT: Origene Technologies, Inc

TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFERENCE: LU 103 RI

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1

SEQ ID NO 72

LENGTH: 547

TYPE: PRT

ORGANISM: Homo sapiens

US-10-164-595-72

Query Match 98.1%; Score 2811; DB 4; Length 547;

Best Local Similarity 98.7%; Pred. No. 3.6e-261; Indels 6; Gaps 1;

Matches 546; Conservative 0; Mismatches 1;

Qy 1 MAASLSRLGLDVLWGKLGRLYPWPWGKI VNPDKLKKPRGKCKFFVKFFGTEDHAWIKVEQL 60

Db 1 MAASLSRLGLDVLWGKLGRLYPWPWGKI VNPDKLKKPRGKCKFFVKFFGTEDHAWIKVEQL 60

Qy 61 KPYHAHKEEMIKINKGRFOQAVDAVEEFLPRAKQDTS SHNSDDKNRNSSEERSRP 120

Db 61 KPYHAHKEEMIKINKGRFOQAVDAVEEFLPRAKQDTS SHNSDDKNRNSSEERSRP 120

Qy 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSEKSGPLKRAQSQSPKRGPRPKDEKD 180

Db 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSEKSGPLKRAQSQSPKRGPRPKDEKD 180

Qy 181 LTIPESSTVKGMMAGPMAAFKWPQTAPEFVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240

Db 181 LTIPESSTVKGMMAGPMAAFKWPQTAPEFVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240

Qy 241 ICEBETGTSIQAADSTAVNGSIITPDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTA 300

Db 241 ICEBETGTSIQAADSTAVNGSIITPDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTA 300

Qy 301 EKCDLFIQEGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 360

Db 301 EK-----EGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 354

Qy 361 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAM 420

Db 355 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAM 414

Qy 421 GKTSPFLGVGNAAKMMLIVNVVQGSFMAITAEGLTLAHTVQSQOQTLLDILNQGLASI 480

Db 415 GKTSPFLGVGNAAKMMLIVNVVQGSFMAITAEGLTLAHTVQSQOQTLLDILNQGLASI 474

Qy 481 FLDDQCKNTLQGNFKPDFLYKYIQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS 540

Db 475 FLDDQCKNTLQGNFKPDFLYKYIQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS 534

Qy 541 DNDMSAVYRAYTH 553

Db 535 DNDMSAVYRAYTH 547

RESULT 2

US-09-364-230-4

Sequence 4, Application US/09364230

Patent No. 6348339

GENERAL INFORMATION:

APPLICANT: Hitze, Rebecca E.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

FILE REFERENCE: BB-1178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT FILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Microsoft Office 97

SEQ ID NO 4

LENGTH: 360

TYPE: PRT

ORGANISM: Zea mays

US-09-364-230-4

Query Match 25.6%; Score 733; DB 4; Length 360;

Best Local Similarity 52.3%; Pred. No. 7.7e-62;

Matches 148; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

Qy 266 TDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTAEKCDLFIQEGARLGRTPAEVWSTCD 325

Db 64 SEMEVGFLGLGIMGKAMATNLLRHGFRVTVVNNRTLAKCQELAAUGATVGETPASVSKCR 123

Qy 326 ITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDMSTVDADTVTELAAQVIVSRGRFLEA 385

Db 124 YTIAMLDSPSAALSVDFDKGVLEQIGSGKGYVDMSTVDATSTKISEAVKQKGAPLEA 183

Qy 386 PVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAMGKTSFPLGEVGNAAKMLIVNVVQGS 445

Db 184 PVSGKXPAEDGQLVILAAAGDKPLYDGMIPAFDVLGKKSFFLGEIGNGAKMLVNVVWVG 243

Qy 446 SFMATIAEGLTLAHTVQSQOQTLLDILNQGLASIFLDQCKNTLQGNFKPDFLYKYIQK 505

Db 244 SMNLSSEGLCLADKSGLSQTLDDLDLGLAIAIMPFLKGPFTMLQGSYSPAFPLKHQOK 303

Qy 506 DLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548

Db 304 DRLALALGDENAVAMPVSAANAANEAFAKRSILGLGDDQDFSAVY 346

RESULT 3

US-09-364-230-8

Sequence 8, Application US/09364230

Patent No. 6348339

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Hitze, William D.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

FILE REFERENCE: BB-1178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT FILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Microsoft Office 97

SEQ ID NO 8

LENGTH: 345

TYPE: PRT

ORGANISM: Glycine max

US-09-364-230-8

Query Match 23.8%; Score 682; DB 4; Length 345;

Best Local Similarity 47.1%; Pred. No. 5.7e-57;

Matches 136; Conservative 54; Mismatches 99; Indels 0; Gaps 0;

Qy 262 SITPTDKKIKGFLGLGMSGIVSNLLKMGHTVTVVNNRTAEKCDLFIQEGARLGRTPAEV 321

Db 46 AVTEPPARIGFLGLGIMGSPMAHNLKAGVDLTVVNNRTSKCDPLISLGAKYKPSPEVA 105

ALIGNMENTS

RESULT 1

US-10-164-595-72

Sequence 72, Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:

APPLICANT: Origene Technologies, Inc

TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFERENCE: LU 103 RI

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1

SEQ ID NO 72

LENGTH: 547

TYPE: PRT

ORGANISM: Homo sapiens

US-10-164-595-72

Query Match 98.1%; Score 2811; DB 4; Length 547;

Best Local Similarity 98.7%; Pred. No. 3.6e-261; Indels 6; Gaps 1;

Matches 546; Conservative 0; Mismatches 1;

Qy 1 MAASLSRLGLDVLWGKLGRLYPWPWGKI VNPDKLKKPRGKCKFFVKFFGTEDHAWIKVEQL 60

Db 1 MAASLSRLGLDVLWGKLGRLYPWPWGKI VNPDKLKKPRGKCKFFVKFFGTEDHAWIKVEQL 60

Qy 61 KPYHAHKEEMIKINKGRFOQAVDAVEEFLPRAKQDTS SHNSDDKNRNSSEERSRP 120

Db 61 KPYHAHKEEMIKINKGRFOQAVDAVEEFLPRAKQDTS SHNSDDKNRNSSEERSRP 120

Qy 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSEKSGPLKRAQSQSPKRGPRPKDEKD 180

Db 121 NSGDEKRLSLSEGKVKKNMGEKKRVSSEKSGPLKRAQSQSPKRGPRPKDEKD 180

Qy 181 LTIPESSTVKGMMAGPMAAFKWPQTAPEFVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240

Db 181 LTIPESSTVKGMMAGPMAAFKWPQTAPEFVKDADPHFHFLLSQTEKPAVCYQAITKKLK 240

Qy 241 ICEBETGTSIQAADSTAVNGSIITPDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTA 300

Db 241 ICEBETGTSIQAADSTAVNGSIITPDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTA 300

Qy 301 EKCDLFIQEGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 360

Db 301 EK-----EGARLGRTPAEVWSTCDITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDM 354

Qy 361 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAM 420

Db 355 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAM 414

Qy 421 GKTSPFLGVGNAAKMMLIVNVVQGSFMAITAEGLTLAHTVQSQOQTLLDILNQGLASI 480

Db 415 GKTSPFLGVGNAAKMMLIVNVVQGSFMAITAEGLTLAHTVQSQOQTLLDILNQGLASI 474

Qy 481 FLDDQCKNTLQGNFKPDFLYKYIQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS 540

Db 475 FLDDQCKNTLQGNFKPDFLYKYIQDLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQS 534

Qy 541 DNDMSAVYRAYTH 553

Db 535 DNDMSAVYRAYTH 547

RESULT 2

US-09-364-230-4

Sequence 4, Application US/09364230

Patent No. 6348339

GENERAL INFORMATION:

APPLICANT: Hitze, Rebecca E.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

FILE REFERENCE: BB-1178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT FILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Microsoft Office 97

SEQ ID NO 4

LENGTH: 360

TYPE: PRT

ORGANISM: Zea mays

US-09-364-230-4

Query Match 25.6%; Score 733; DB 4; Length 360;

Best Local Similarity 52.3%; Pred. No. 7.7e-62;

Matches 148; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

Qy 266 TDKKIGFLGLGMSGIVSNLLKMGHTVTVVNNRTAEKCDLFIQEGARLGRTPAEVWSTCD 325

Db 64 SEMEVGFLGLGIMGKAMATNLLRHGFRVTVVNNRTLAKCQELAAUGATVGETPASVSKCR 123

Qy 326 ITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDMSTVDADTVTELAAQVIVSRGRFLEA 385

Db 124 YTIAMLDSPSAALSVDFDKGVLEQIGSGKGYVDMSTVDATSTKISEAVKQKGAPLEA 183

Qy 386 PVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAMGKTSFPLGEVGNAAKMLIVNVVQGS 445

Db 184 PVSGKXPAEDGQLVILAAAGDKPLYDGMIPAFDVLGKKSFFLGEIGNGAKMLVNVVWVG 243

Qy 446 SFMATIAEGLTLAHTVQSQOQTLLDILNQGLASIFLDQCKNTLQGNFKPDFLYKYIQK 505

Db 244 SMNLSSEGLCLADKSGLSQTLDDLDLGLAIAIMPFLKGPFTMLQGSYSPAFPLKHQOK 303

Qy 506 DLRLAIALGDVAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548

Db 304 DRLALALGDENAVAMPVSAANAANEAFAKRSILGLGDDQDFSAVY 346

RESULT 3

US-09-364-230-8

Sequence 8, Application US/09364230

Patent No. 6348339

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Hitze, William D.

APPLICANT: Kinney, Anthony J.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

FILE REFERENCE: BB-1178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT FILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Microsoft Office 97

SEQ ID NO 8

LENGTH: 345

TYPE: PRT

ORGANISM: Glycine max

US-09-364-230-8

Query Match 23.8%; Score 682; DB 4; Length 345;

Best Local Similarity 47.1%; Pred. No. 5.7e-57;

Matches 136; Conservative 54; Mismatches 99; Indels 0; Gaps 0;

Qy 262 SITPTDKKIKGFLGLGMSGIVSNLLKMGHTVTVVNNRTAEKCDLFIQEGARLGRTPAEV 321

Db 46 AVTEPPARIGFLGLGIMGSPMAHNLKAGVDLTVVNNRTSKCDPLISLGAKYKPSPEVA 105

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QY 322 STCDITACVSDPXAADLVLPSPVLOQIRPGKCYVDMSTVDADTVTELAQVIVSRGGR 381
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
106 ASCDVTFAMLADPQSAVDVACGKGAANGMGPGKYVDVSTVDGDTKLINGHMKSTGAL 165
QY 382 FLEAPVSGNQLSNDGMLVILAAAGDRGLYEDSCSFQAMGKTSFELGVEGNAAKMMLIVN 441
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
166 FLEAPVSGKPKAPDGGQLIFATAGDKNLYEAVGSLDDIMGSKFYLDGVDGNGAAMKLIVN 225
QY 442 MVQGSFMATIAEGTLTAHVTSQSQTLLDILNOGOLASIFLDQKQNTLQGNFKPDPFLK 501
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
226 MIMSMWASFSBGLLSEKVGLDPDVLVQVVSQGAISAPMYSTKGPSMIQSLYPTAPFLK 285
QY 502 YIQKDLRLAIALGDVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
286 HQKDLRLAIALGAEVSQPTPIASAAANELYKVAKSNGLSDQDFSAVIEA 334

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RESULT 4

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US-09-364-230-2
; Sequence 2, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; EARLIER APPLICATION NUMBER: 1999-07-29
; EARLIER FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (244)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)
US-09-364-230-2

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Query Match 18.8%; Score 537.5; DB 4; Length 247;
Best Local Similarity 45.3%; Pred. No. 2.5e-43;
Matches 106; Conservative 47; Mismatches 80; Indels 1; Gaps 1;

QY 284 SNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVWSTCDITFACVSDPXAADLVLG 343
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
2 SNLIRAGCDVTVNRTKCDPLLSLGAKVEPTPAQVASSCDVTFAMLADPQSAAEVACG 61
QY 344 PSGLVQGRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQLSNDGMLVILA 403
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
62 SSGAAEGLAPGKYVDVSTVDGATSKLIGERTITSTGASFLAPVSGSKPKPAEDGLLIFLT 121
QY 404 AGDRGLYEDSCSFQAMGKTSFELGVEGNAAKMMLIVNMQGSFMATIAEGTLTAHVTSQ 463
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
122 AGDESLYKRVAPLDDVMGKSFYLDGVDGNGAAMKLIVNVMGSMVVSFSEGLLSEKVL 181
QY 464 SQOTLLDILNOGLASIFLDQKQNTLQGNFKPDPFLKYIQKDLRLAIALGDV 517
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
182 DPTLVEVISQGAISAPFSLKGPSWKAAYPPAPFLKHQQKDLSS-SIGLADRV 234

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RESULT 5

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US-09-489-039A-9294
; Sequence 9294, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

```

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; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9294
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9294

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Query Match 12.7%; Score 364; DB 4; Length 307;
Best Local Similarity 28.7%; Pred. No. 1.7e-26;
Matches 81; Conservative 60; Mismatches 139; Indels 2; Gaps 1;

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QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVWSTCDITF 328
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
15 KVGFIGIGIMGPKMSKNLLKAGYSLVVSNDPNAIADVIAAGAEATATTPKAIAEQCEVII 74
QY 329 ACVSDPKAAKDLVLGSPGVLOQIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
75 TLPNSPHVQEVALLGNGIIEGAKPGTVVIMDSIAPLASREISEALKAGIDMLDAPVS 134
QY 389 GNQOLSDNGMLVILAAAGDRGLYEDSCSFQAMGKTSFELGVEGNAAKMMLIVNMQGSFM 448
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
135 GGEPKAIDGTLVSVVGDKAIFDKYDLMKAMAGSVVHTGDIAGNVTKLANQVIVALNI 194
QY 449 ATIAEGLTLAHVTSQSQTLLDILNOGOLASIFLDQKQNTLQGNFKPDPFLKYIQKDLR 508
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
195 AAMSEALTATKAGVNPDLVIYQIRGLAGSTVLDKAPWMDRNFKPGPRIDLHKDLA 254
QY 509 LAILALGDVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
255 NALDTSHGVGALPLTAAVVMQALRADGLGTADHSHALACY 296

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RESULT 6

```

US-09-328-352-7407
; Sequence 7407, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7407
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7407

```

```

Query Match 12.0%; Score 343.5; DB 4; Length 299;
Best Local Similarity 28.1%; Pred. No. 1.5e-24;
Matches 79; Conservative 56; Mismatches 145; Indels 1; Gaps 1;

```

```

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVWSTCDITF 328
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
12 RIGFVGTGIMGPMAMNLLKAGHQIKWNRTSSKAESEKAGAHVCSSELEQIGKDVDFLI 71
QY 329 ACVSDPKAAKDLVLGSPGVLOQIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
72 CMLSDGKICNEILFQERGAISQLPESTVIWMSIPVEVAKTQSEKCKERGILYLDAPVS 131
QY 389 GNQOLSDNGMLVILAAAGDRGLYEDSCSFQAMGKTSFELGVEGNAAKMMLIVNMQGSFM 448
Db :||:||||:||||:| :||:||||:||||:| :||:||||:||||:| :||:||||:||||:|
132 GGEKGAQNASLAIMVGGDAQTFSHAHVLSAMGR--PILVGEVCGMLAKLVNQIVASTI 190

```

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5109:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...299
SEQUENCE DESCRIPTION: SEQ ID NO: 5109:
US-09-107-532A-5109
Query Match 11.9%; Score 340; DB 4; Length 299;
Best Local Similarity 28.8%; Pred. No. 3.2e-24;
Matches 76; Conservative 52; Mismatches 136; Indels 0; Gaps 0;
QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVYSTCDITF 328
DB 6 KLGFTGTGVMGSAVARHLLLEAGHEAVVNRKAKADPLVTEGAIWADTFKVAEQSNILF 65
QY 329 ACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDMSTVDADTVTBLAQVTVSRGGRFLEAPVS 388
DB 66 TWVGYPKDVEEIIYGGSGIFSDISGHILVLDLTSTPSLAEKIATKAKEKGADALDAPVS 125
QY 389 GNOQLSNDGMLVILAAGRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLI VNMVQGSF 448
DB 126 GGDGLGAKNGTLTIMVGGEAVYDVLPLPKFEGTFTTTLHGSAGKQHTKMANQIMAGTM 185
QY 449 ATIAEGLTLAHTVGTGSOQTLLDLNQGQLASIFLDQKCNILQGNFKPDPFYLYKIQKDLR 508
DB 186 TGNTMLVYAKNGLDLKKVIETLSSGSAANWSLNSYSPRIKEDYTPGFFVKHFIDK 245
QY 509 LAIALGDVAVNHTPMAAANAEVYK 532
DB 246 IALEEAEKMDLVLPATTOALKLYE 269

RESULT 9

US-09-252-991A-27650
Sequence 27650, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27650
LENGTH: 543
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27650
Query Match 12.0%; Score 343; DB 4; Length 543;
Best Local Similarity 23.5%; Pred. No. 4.4e-24;
Matches 113; Conservative 83; Mismatches 212; Indels 72; Gaps 11;
QY 110 RNSSEERSRNSGDEK-----KLSLSE---GKVKKNMGCKRVSS-----GSSERGSK- 157
DB 91 RROAGSRHPHGGDQHPHRLPAPHPGPGDPRGROQRPVPAIRHLSHADHGRPP 150
QY 158 -----SPLKRAEQSPKRGRRP-----KDEKDLTIPESSTVKGMMGMAAFKMQPTAS 207
DB 151 GHPGKPVGGDQPRATRRQPRPRTHRRDQLPL----- 184
QY 208 BPVKDADPH-----FHHLLSQTEKPAVCYQATYKLIKIBETGTSIQAA 254
DB 185 -PLRAGPGHRLPGLDLRLRVQAGHH-----RSRPLRDEDAQRLIRTHEQDAPASLRGAT 238
QY 255 DSTAVNGSITPDKKIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARL 313
DB 239 RQTEPGDTLM---AKIGFTGTGIMGKPMQAQNLQKAGHSLFUSTHDDAAPADL-LEAGAIA 294
QY 314 GRTPAEVYSTCDITFACVSDPKAAKDLVLGPGSVLQGIKPGKCYVDMSTVDADTVTBLAQ 373
DB 295 LANPEVAQAEFIIVWPDFTQVEDVLPKDGIAEGVGPNKVVDMSSISPTATKFAE 354
QY 374 VIVSRGGRFLEAPVSGNQLSNDGMLVILAAGRGLYEDCSSCFQAMGKTSFFLGEVGN 433
DB 355 KIKATGAQVLDAPVSGGEGVGAKAATLSIMVGGCPNSFERALPLFQAMGNHITRVGNGD 414
QY 434 AKMWLI VNMVQGSFMTIAEGLTLAHTVGTGSOQTLLDLNQGQLASIFLDQKCNILQGN 493
DB 415 QTKAVANQIIVAINLQAVAEALFLFAARNGADPAKVEALMGFPASSRILLEVGERNVKGT 474
QY 494 FKPDFYLYKIQKDLRLAIALGDVAVNHTPMAAANAEVYKAKALDOSDNDMSAVRAYTH 553
DB 475 FDPGFRISLHQDLNLALAGARENLNLEPNTANAQVFTCAAGISGNDHDSALIKGLEH 534

RESULT 8
US-09-107-532A-5109
Sequence 5109, Application US/09107532A
Patent No. 6583275

US-09-489-039A-9424
 ; Sequence 9424, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 9424
 ; LENGTH: 304
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-9424

Query Match 11.4%; Score 326; DB 4; Length 304;
 Best Local Similarity 29.9%; Pred. No. 7.4e-23;
 Matches 88; Conservative 52; Mismatches 136; Indels 18; Gaps 5;
 QY 266 TDK-----KIGFLGGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEV 320
 Db 11 TDKMTTPKVAVLGLGAMGHAFASNLLKNGFTVAGWNSPARGEDLOAHGLSLHATPOQA 70
 QY 321 VSTCDITFACVSDPKAAKDLVLGSPGVLOQIRPGKCYVDMSTVDADTVTELAAQVI----- 375
 Db 71 VADAEVILMLADEATELVL---AQAPACQPAIYQMGTTIG---LPETROAIALLRE 124
 QY 376 VSRGGRFLEPVSNGQOLSDNDMLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAK 435
 Db 125 LQPAITYVIDAPVSGTKAPAEKAQILVLASGDREKGAAPVFAISRGTFQWFGAGNSQK 184
 QY 436 MMLIVANVQSGFWATTAEGLTLAHVTGSGQOQLDILNQGLASIFLDQCKQNTILQGNFX 495
 Db 185 MKLIVLNAWLISMQGAESAQLAKTLGFTPDQLMSALEGGFLAAPPYVVKVLDALASEQFT 244
 QY 496 PDFYLYKIQKDLRLALALGDAVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYR 549
 Db 245 PQWLAHALKADRLALSLEAP--HTMPELENIAELWQQAADAGYAGEDLSAVYQ 296

RESULT 10
 US-09-252-991A-26001
 ; Sequence 26001, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 26001
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-26001

Query Match 11.3%; Score 324.5; DB 4; Length 324;
 Best Local Similarity 26.5%; Pred. No. 1.1e-22;
 Matches 74; Conservative 62; Mismatches 142; Indels 1; Gaps 1;
 QY 270 IGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGA-RLGRTPAEVVSTCDITF 328
 Db 40 VAFGLGTMGYPMAGHLQREGDVCVYNNSSAKALRWVEYAGRRADTPREACAGAEVLF 99

QY 329 ACVSDPKAAKDLVLGSPGVLOQIRPGKCYVDMSTVDADTVTELAAQVIYVSRGGRFLEAPVS 388
 Db 100 CCVGNDDDLRAVALGEGQAFAGMAPGSLFVDHTTASAEVARELSLLAAARELGFLEAPVS 159
 QY 389 GNOQLSDNDGMLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIVNVQSGSPM 448
 Db 160 GGAGAVNGALTVMVGSEAEYRAEPLLRYSARMVRKMGDVGSQLTVMVNCICVAGLL 219
 QY 449 ATIAEGLTLAHVTGSGOQTLDDIILNQGLASIFLDQCKQNTILQGNFKDPDFYLYKIQKDLR 508
 Db 220 QGLAEALHFARCAGLDGEAAMQVIGKGAASQWLENHQSLMAGEFDFGFAVDNMRKDL 279
 QY 509 LAIALGDAVNHPTPMAAAANEVYKRAKALDOSDNDMSAV 547
 Db 280 ILLAEARRNGAQLPVTALVDQFYAEVQAMGGGRWDTSSL 318
 RESULT 11
 US-09-252-991A-17923
 ; Sequence 17923, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 17923
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-17923

Query Match 10.8%; Score 310; DB 4; Length 330;
 Best Local Similarity 28.6%; Pred. No. 2.9e-21;
 Matches 83; Conservative 57; Mismatches 136; Indels 14; Gaps 6;
 QY 270 IGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDITFA 329
 Db 42 LAFAGLGLMGVPMCRRLAAGYPLAVNRSFGKRELLAEGAKAVEVPAELAADEILML 101
 QY 330 CVSDPKAAKDLVLGSPGVLOQIRPGKCYVDMSTVDADTVTELAAQVIYVSR-GGRFLEAPVS 388
 Db 102 CIADTAARVREVFAGGIVENAEFGQLLVDFSSAEPAATREMAAELEARGCVRWVDAPVS 161
 QY 389 GNOQLSDNDGMLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIVNVQSGSPM 448
 Db 162 GGTPGAESGSLAIMGAGRAADIERLRPLVLSRLGRLTRMGV-AGQVTKVCNQ-----M 215
 QY 449 ATIAEGLTLAHVTGSGOQTLDDI-LNQGLASIFLDQCKQNTIL-----QCNFKP-DFYLYK 501
 Db 216 IVACNALVIAEVVVALAEAGVDASLVAPALAGFADSKPLQILAPQWAEBSRVEPVKWHVR 275
 QY 502 YIQKDLRLALALGDAVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYR 551
 Db 276 TILKDLDTAVKLSREGQAATPMGSLAAQLMRLHSGQGLYLERDPATLIVEQY 325

RESULT 12
 US-09-711-164-438
 ; Sequence 438, Application US/09711164
 ; Patent No. 6589738
 ; GENERAL INFORMATION:
 ; APPLICANT: Forsyth, R. Allyn
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith

; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
 ; FILE REFERENCE: ELITRA.008A
 ; CURRENT APPLICATION NUMBER: US/09/711.164
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/164415
 ; PRIOR FILING DATE: 1999-11-9
 ; NUMBER OF SEQ ID NOS: 469
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 438
 ; LENGTH: 292
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-09-711-164-438

Query Match 10.2%; Score 301.5; DB 4; Length 292;
 Best Local Similarity 27.7%; Pred. No. 1.6e-20;
 Matches 78; Conservative 51; Mismatches 152; Indels 1; Gaps 1;
 ;
 QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
 Db 2 KLGFIGLIGMTPTMAINARAGQJHV-TTIGPVADLLSLGAVSETARQVTEASDIIF 60
 ;
 QY 329 ACVSDPKAAKDLVLPSPGVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
 Db 61 IMVPTPQVEVLFGENCCTKSLKGTIVDMSSISPIETKRFARQVNNELGQDYLDAFVS 120
 ;
 QY 389 GNQQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGEVGNAAKMLIVNVQGSFM 448
 Db 121 GGEIGAREGTLIMVGGDEAVFERVKPLFELLGKNITLIVGGNGDQCTCKVANQIIVALNI 180
 ;
 QY 449 ATTAGLTLAHVTGOSQQTLLDILNOGQLASIFLDKQCNILQGNFKPDPFVLYKXIQDLR 508
 Db 181 EAVSALLFASKAGADPVRVQALMGGFASRILEVHGEMIKRTPNFPGFKIALHQKDLN 240
 ;
 QY 509 LAIALGDVANHPTMAAAANEVYKRAKALDQSDNDMSAVYRA 550
 Db 241 LALQAKALNLPNTATCQELFNTCAANGSGQLDHSALVQA 282

RESULT 13
 US-09-252-991A-24727
 ; Sequence 24727, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24727
 ; LENGTH: 295
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-24727

Query Match 10.2%; Score 291; DB 4; Length 295;
 Best Local Similarity 28.9%; Pred. No. 1.6e-19;
 Matches 82; Conservative 57; Mismatches 135; Indels 10; Gaps 5;
 ;
 QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVST---CD 325
 Db 6 KVGFLGLGGGAAMATFLVQAGLEVTVNRSAAACEPLV---ALGAARAEVGDLFGLD 61
 ;
 QY 326 ITFACVSDPKAAKDLVLPSPGVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEA 385
 Db 62 VVISMLADQAIRGLI-DSGALERARPGIHLMSMTLSLDCVEALDQAHQROGLAFVAA 120

QY 386 PVSNGOQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGEVGNAAKMLIV-NMVQ 444
 Db 121 PVFGRTDVAEAGKLNIVVGGPEBAIEQVKALLEIMGQKTFWFGKDPGRGAMAVKISGNFMI 180
 ;
 QY 445 GSWATTIAGLTLAHVTGOSQQTLLDILNOGQLASIFLDKQCNILQGNFKP-DFVLYKYI 503
 Db 181 ASATIESMGESVALVKRLGVGFGRFMEIWSSTLFDAPVYRNVGPOIVFQRTTPARFRLVIG 240
 ;
 QY 504 QKDLRLAIALGDVANHPTMAAAANEVYKRAKALDQSDNDMSAV 547
 Db 241 LKQVDLALSAGKRHNVPDPLASLLHDVLLERAIHAHGDGEDSDWTAL 284

RESULT 14
 US-09-328-352-4879
 ; Sequence 4879, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 4879
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-4879

Query Match 10.0%; Score 287.5; DB 4; Length 303;
 Best Local Similarity 25.5%; Pred. No. 3.7e-19;
 Matches 74; Conservative 55; Mismatches 154; Indels 7; Gaps 2;
 ;
 QY 270 IGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDITFA 329
 Db 10 IAFIIGLGNMGRMAQNLKAGLVYGYDLSEVAIOHFAAGGIVCDSPQNAAKQADVIT 69
 ;
 QY 330 CVSDPKAAKDLVLPSPGVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
 Db 70 MIPAARKHVEVLGNGVLEVLKAGSLCIDSITDPIQKIDIAVAQSKNIKICDAPVSG 129
 ;
 QY 390 NOQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGEVGNAAKMLIVNVQGSFVA 449
 Db 130 GTIGQAAGTLTPMVCADQTFNEVPVLSHMGKNIVHCGDVAGGQIATKCNLLILGISMA 189
 ;
 QY 450 TTAGLTLAHVTGOSQQTLLDILN--QGQLASIFLDKQCNILQGNFKPDPFVLYKY 502
 Db 190 AVAEGNALGVKLGIDPQALAGVINTSSGRCWSSDVCNPNPHINENAPASRGYQDGFATQL 249
 ;
 QY 503 IQKDLRLAIALGDVANHPTMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
 Db 250 MLKDLGLAVEAAGVQKQPVLLGGMVQQLYQCMRGNALHDFSIIQQYL 299

RESULT 15
 US-09-328-352-8139
 ; Sequence 8139, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 8139
 ; LENGTH: 326
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-8139

Query Match
Best Local Similarity 9.3%; Score 266; DB 4; Length 326;
Matches 78; Conservative 42; Mismatches 122; Indels 28; Gaps 6;

QY 270 IGFLGLGMSGIVSNLLKMGHTVTVNRTAKCDLFTQEGA-----RLGRTPAEVVST 323
DB 47 IAFGLGLGMSGRMARLLTQAGPQVAVNRRTTSACEELDIGAHALDLSNIGQYP----- 100

QY 324 CDITFACVSDPKAAKDLVLGSPGVQGIIRPGKCYVDMSTVDADTVELAQIVSRGRFL 383
DB 101 --LILTCLADDKAVQAVF---DQITNLKAGQIVDFSSLSVAATKALQAASODVTWI 155

QY 384 EAPVSGNQLNDGMLVILAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAKMLVNVV 443
DB 156 DSPVSGGTGAEQGTFLVFAGGDAQTIEALSPVYNLSQVTRMGDTGTGQATKICNQLI 215

QY 444 QGSPMATIAGLTLAHVTGQSQOQLDILINOGQLASIFLDKQCNIL-----QGNFKP-D 497
DB 216 VAANSALIAEVALADRAVDVTTLLAPALAG-----PADSKPQILAPRMATHTFEPVQ 270

QY 498 FYLKYIQKDLRLALALGDAVNHPMPMAAA 527
DB 271 WKVQTLKDLNNVATLANNVNDIPVAKA 300

RESULT 16
US-09-364-230-6
; Sequence 6, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; EARLIER FILING DATE: 1999-07-29
; EARLIER FILING DATE: 60/094,990
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-364-230-6

Query Match
Best Local Similarity 9.0%; Score 258.5; DB 4; Length 342;
Matches 81; Conservative 43; Mismatches 159; Indels 37; Gaps 6;

QY 256 STAVNGSITPTDKKIGLGLGMSGIVSNLLKMGHTVTVNRTAKCDLFTQEGARLGR 315
DB 25 SAHVOSQL-----ENVGFIGLGNAGMARNLNMGVYKVTVDVNTMTKKFSDGIPTKL 80

QY 316 TPAEVVSTCDITFACVSDPKAAKDLVLGSPGVQGIIRPGKCYVDMSTVDADTVE 370
DB 81 SPLEVSXSSDVITMLPSSAHVLDVYNGRGLLAN---GGCLGPMYIDSPVDPQTSRK 137

QY 371 LAQVI-----VSRGRFLEAPVSGNQLNDGMLVILAGDRGLYEDCSCFOAM 420
DB 138 ISMDISRCTLKBKPYAEKPMMLDAPVGGVPPAEAGKLTFLVGGSEAYLAANPLLISM 197

QY 421 GXTSPFLGVBGNAKMLVNVVQSGFMATIAEGLTLAHVTGQSQOQLDILIN----- 473
DB 198 GKTYICGAGNGSVAKICNNMANGISMLGVSEAFALGQNLGKASVLTDFNCSSARCW 257

QY 474 -----QGQLASIFLDKQCNILQGNFKPDPFLYKIQKDLRLALALGDAVNHPMPMAAA 529
DB 258 SSDTYNPPGVNMDVPSR-----NYDGGFTSKMLTKDLDLAWASAGVGNCPFGSQALE 313

QY 530 VYKRAKALDQSDNDMSAVYR 549
DB 314 IYKLCADGCELDKDFSCAPR 333

RESULT 17
US-09-134-000C-5460
; Sequence 5460, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5460
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5460

Query Match
Best Local Similarity 8.8%; Score 252; DB 4; Length 247;
Matches 58; Conservative 41; Mismatches 118; Indels 0; Gaps 0;

QY 316 TPAEVVSTCDITFACVSDPKAAKDLVLGSPGVQGIIRPGKCYVDMSTVDADTVELAQVI 375
DB 1 TPKAIAEASDIIITMVGSPSDVEGVFENETGIFQADLTGKIVVDLTSTPTLAEKIAKKA 60

QY 376 VSRGRFLEAPVSGNQLNDGMLVILAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAK 435
DB 61 AEVGAHALDAPVSGGDLGAKNGTLTIMGVGDQESYDTVLPIFTGKTFMLHGSAGKGQH 120

QY 436 MMLIVNVQSGFMATIAEGLTLAHVTGQSQOQLDILINOGQLASIFLDKQCNILQGNFK 495
DB 121 TKMANQLMIAGTMTGLTLMVYANATGLTLEKVLTVGGSSAANWSLSNYGPRILKEDYT 180

QY 496 PDFLYKIQKDLRLALALGDAVNHPMPMAAAANEVYK 532
DB 181 PGFFVNFHFKDLKALDEAKKLDLPLEATQKATELYE 217

RESULT 18
US-09-364-230-12
; Sequence 12, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; EARLIER FILING DATE: 1999-07-29
; EARLIER FILING DATE: 60/094,990
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (154)
; FEATURE:
; NAME/KEY: UNSURE

Db 172 YRIGSDIGLSTVKIHHQLLAGVHIAVAEAMALAAARAGIPLTMYDVVTHAAGSNWME 231
Qy 484 QKQNTILQGNFKPDPYLYKIQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDND 543
Db 232 NRMQHVLDGDSYSPKSAVDIEVKDLGLVNDTARALTPLPLATTALNMFTSASNAGFGRED 291
Qy 544 MSAYRAY 551
Db 292 DSAVIKIF 299

Query Match 8.4%; Score 240.5; DB 4; Length 350;
Best Local Similarity 26.1%; Pred. No. 1.5e-14;
Matches 80; Conservative 41; Mismatches 166; Indels 19; Gaps 6;

265 PTDKIGLGLGMLGSGIVSNLLKMGHTVTYNNRTAEKCDLFIQEGARLGRTPAEVYSTC 324
Db 38 PHMESVGFGLGNMGSHMARNLVRAGYRVSVDINEVAMKFSDDGIPTRKSPLEVSSESS 97
Qy 325 DITFACVSDPKAAKDLVLGSGVL-QGIRPK-CYVDMSTVDADTVTELAQ-----VIVS 377
Db 98 DVVITMLPSSAHVLDVYSGRLLGNGRGLPWLIDYSTVDPTSRKISMDSMRCKLINE 157
Qy 378 RGR-----FLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAMGKTSFFLGEVGN 432
Db 158 KKGVAEKPIMDAPVPGGXPKAKVGHXXXXXXXKXXXXXXXXXXLLANGKKLIYCGGAGN 217
Qy 433 AAKMMLIVNVVQGSFMATIAEGLTLAHVTGQSQQTLDLINOGQLASIFLD--QKQNIL 490
Db 218 GSAKLCNNMAWISMLGVSEAFALGQNLGKASTLTDIENCSSARCWSSDTYNPVPQVM 277
Qy 491 QG-----NFKPDPYLYKIQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDNDS 545
Db 278 TGVPSRNVYDGGFTSKLMAKDLIDLAMASAGVGVKCPMGSEALEYTKLDEGCEFFKDFS 337
Qy 546 AVYRAY 551
Db 338 CAPRHF 343

RESULT 19
US-09-489-039A-9860
; Sequence 9860, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9860
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9860

Query Match 7.9%; Score 226.5; DB 4; Length 309;
Best Local Similarity 22.4%; Pred. No. 2.7e-13;
Matches 69; Conservative 64; Mismatches 160; Indels 15; Gaps 6;

Qy 249 TSIQAADSTAVNGSITPTDKKIGLGLGMLGSGIVSNLLKMGHTVTW--NRTAEKCDLF 306
Db 2 TNVHKTSMHAHTNVC-----VIGLSGMGAARACLOAG--LNTWGVNDINPDCRAL 52
Qy 307 IOEGARLGRTPAEV--VSTCDITFACVSDPKAAKDLVLGSGVLQIRPKCYVDMSTVD 364
Db 53 LAAGAK-GAGPSAVPFAAEALDAVLLVNAQAQVRGILFGESGLAAHLKPGTVVMVSSSTIA 111
Qy 365 ADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAMGKTS 424
Db 112 SADAQALAEALAEYQLMLDPAFVSGGAVKAAAGMTVMASGDAAFARLAPVLDAVAGKV 171
Qy 425 FFLG-EVGNAAKMWLIYNNVQGSFMATIAEGLTLAHVTGQSQQTLDLINOGQLASIFLD 483
Db 172 YRIGSDIGLSTVKIHHQLLAGVHIAVAEAMALAAARAGIPLTMYDVVTHAAGSNWME 231
Qy 484 QKQNTILQGNFKPDPYLYKIQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDND 543
Db 232 NRMQHVLDGDSYSPKSAVDIEVKDLGLVNDTARALTPLPLATTALNMFTSASNAGFGRED 291
Qy 544 MSAYRAY 551
Db 292 DSAVIKIF 299

Db 172 YRIGSDIGLSTVKIHHQLLAGVHIAVAEAMALAAARAGIPLTMYDVVTHAAGSNWME 231
Qy 484 QKQNTILQGNFKPDPYLYKIQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDND 543
Db 232 NRMQHVLDGDSYSPKSAVDIEVKDLGLVNDTARALTPLPLATTALNMFTSASNAGFGRED 291
Qy 544 MSAYRAY 551
Db 292 DSAVIKIF 299

RESULT 20
US-09-489-039A-11448
; Sequence 11448, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11448
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11448

Query Match 7.8%; Score 224.5; DB 4; Length 309;
Best Local Similarity 22.4%; Pred. No. 4.3e-13;
Matches 69; Conservative 63; Mismatches 161; Indels 15; Gaps 6;

Qy 249 TSIQAADSTAVNGSITPTDKKIGLGLGMLGSGIVSNLLKMGHTVTW--NRTAEKCDLF 306
Db 2 TNVHKTSMHAHTNVC-----VIGLSGMGAARACLOAG--LNTWGVNDINPDCRAL 52
Qy 307 IOEGARLGRTPAEV--VSTCDITFACVSDPKAAKDLVLGSGVLQIRPKCYVDMSTVD 364
Db 53 LAAGAN-GAGPSAVPFAAEALDAVLLVNAQAQVRGILFGESGLAAHLKPGTVVMVSSSTIA 111
Qy 365 ADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAAGDRGLYEDCSCFQAMGKTS 424
Db 112 SADAQALAEALAEYQLMLDPAFVSGGAVKAAAGMTVMASGDAAFARLAPVLDAVAGKV 171
Qy 425 FFLG-EVGNAAKMWLIYNNVQGSFMATIAEGLTLAHVTGQSQQTLDLINOGQLASIFLD 483
Db 172 YRIGSDIGLSTVKIHHQLLAGVHIAVAEAMALAAARAGIPLTMYDVVTHAAGSNWME 231
Qy 484 QKQNTILQGNFKPDPYLYKIQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDND 543
Db 232 NRMQHVLDGDSYSPKSAVDIEVKDLGLVNDTARALTPLPLATTALNMFTSASNAGFGRED 291
Qy 544 MSAYRAY 551
Db 292 DSAVIKIF 299

RESULT 21
US-09-252-991A-22003
; Sequence 22003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18


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, PRIOR APPLICATION NUMBER: US 60/094,190
, PRIOR FILING DATE: 1998-07-27
, NUMBER OF SEQ ID NOS: 33142
, SEQ ID NO 22003
, LENGTH: 221
, TYPE: prt
, ORGANISM: pseudomonas aeruginosa
US-09-252-991A-22003

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Query Match	7.3%	Score 208;	DB 4;	Length 221;
Best Local Similarity	27.5%;	Pred. No. 9.5e-12;		
Matches	53;	Conservative 36;	Mismatches 104;	Indels 0;
Gaps	0;			
QY	270	IGFGLGLMGSGIIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVTVTCDDITFA	329	
Db	9	IAFLGLGNMGSPMAANLLKAGHRVNVFDLQPKAVLSLVEQAGADSAALOCEGAEEVIS	68	
QY	330	CVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTFLAGVIVSRGRGRFLPEAPVSG	389	
Db	69	MLPAGQHVESLYLGDGGLARVAGKPLLLDCSTTAPETARKVAEAAAKGLTLDDAPVSG	128	
QY	390	NQQLSNDGMLVILAAGDRGLYEDSCSCFCQAMCKTSFFLGEVGNAAKMLIVNVQGSFMA	449	
Db	129	GVGGARAGTTSFVCGGPAEGFARARPVLENNGRNIFHAGDHGACQVAKICNNMLLGLIMA	188	
QY	450	TTAEGTLAHVTG	462	
Db	189	GTAEALALGVKNG	201	

RESULT 22
US-08-760-745-5
Sequence 5, Application US/08760745
Patent No. 5972658
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Lyrna K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08760,745
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0169 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

```

; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 945419
US-08-760-745-5

      6.5%; Score 185.5; DB 2; Length 237.
Best Local Similarity 29.8%; Pred. No. 1.5e-09;
Matches 65; Conservative 32; Mismatches 94; Indels 27

Qy 7 RGLDLVWGKLGIRYPWPWGKIVNPPDLKKPRGKCCFFVFFGFGEDHAWIKVE
Db 11 KCGDLVFAKMGYPHWPARIDEMPEAAVKSTANK-YQVFFFGFHTAFLGPK
Qy 67 KEEMIKINKGRFQAVDAVEEFLPRAKGDQDTSSHNSDDKNRRNSSEBSRS
Db 70 KEKFGKPKRRGFSEGLWEIEN-----NPTVASGYQSSQKKSCAAEPVEYEP
Qy 127 RKLSLSEGKVKKNMGEGKRVSSGSGSERGSKSPLKR---AQEQSPRKRGPRP
Db 125 KKGS-AEGSSD---EGKLVIDEPAKEKNEKTLKRRAGDVLDSPR-----
Qy 178 EKDLTIPESSTVKGMMGPMFAAFKWQPTASEPVKQADP 215
Db 177 EED---KEIAALEGERHILFVEVEK-NSTPSEPDSGOGP 210

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RESULT 23
US-08-760-745-3
; Sequence 3, Application US/08760745
; Patent No. 5972658
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Svyra K.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,745
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0169 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 598956
; US-08-760-745-3

```

Query Match 6.5%; Score 185.5; DB 2; Length 240;
 Best Local Similarity 29.8%; Pred. No. 1.6e-09;
 Matches 64; Conservative 30; Mismatches 100; Indels 21; Gaps 8;

QY 7 RLGLVWGLGRYPWPVKIVNPPKDLKPRGKCFVVKFFGTEDHAWIKVQELKPYHAH 66
 DB 11 KGDLVFAKMGYPHWPARDIDDAAGAVKPPNK-YPIFFGTHTAFLGPKDLFFVEES 69
 QY 67 KEEMIKKGRFOQAVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRNSGDEK 126
 DB 70 KEKFGKPKRGFSEGLWEIEN-----NPTVKASGYOSSQKSCVPEPEPEAEAGDGD 124
 QY 127 KLSLSEGVKKNMGEGKKRRVSSGSSGSKSPKRAQ-----EQSPR--KGRPPKDEKD 180
 DB 125 KK-GNAEGSSDE---EGKLVIDEPAKEKNEKALKRRAGDILLEDSPKRPKEAENPEGEE- 179
 QY 181 LTIPESSTVKGMAGPMAAFKMQPTASEPVKDADP 215
 DB 180 ---KEATLEVERPLPMEVEK-NSTPSPGSGRGP 210

RESULT 24
 US-08-760-745-1
 ; Sequence 1, Application US/08760745
 ; Patent No. 5972458
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Suya K.
 ; APPLICANT: Murry, Lynn E.
 ; TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/760,745
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0169 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: lungast01
 ; CLONE: 876242
 ; US-08-760-745-1

Query Match 6.2%; Score 178.5; DB 2; Length 235;
 Best Local Similarity 29.6%; Pred. No. 7.1e-09;
 Matches 63; Conservative 30; Mismatches 99; Indels 21; Gaps 8;

QY 9 GDLVWGLGRYPWPVKIVNPPKDLKPRGKCFVVKFFGTEDHAWIKVQELKPYHAHKE 68
 DB 8 GDLVFAKMGYPHWPARDIDDAAGAVKPPNK-YPIFFGTHTAFLGPKDLFFVEESKE 66
 QY 69 EMIKINKGRFOQAVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRPNNSGDEK 128
 DB 67 KFGKPKNRKGFSEGLWEIEN-----NPTVKASGYOSSQKSCVPEPEPEAEAGDGD 121
 QY 129 LSLSEGVKKNMGEGKKRRVSSGSSGSKSPKRAQ-----EQSPR--KGRPPKDEKD 182
 DB 122 -GNAEGSSDE---EGKLVIDEPAKEKNEKALKRRAGDILLEDSPKRPKEAENPEGEE- 174
 QY 183 IPESSTVKGMAGPMAAFKMQPTASEPVKDADP 215
 DB 175 -KEATLEVERPLPMEVEK-NSTPSPGSGRGP 205

RESULT 25
 US-09-364-230-10
 ; Sequence 10, Application US/09364230
 ; Patent No. 6348339
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Rebecca E.
 ; APPLICANT: Hitz, William D.
 ; APPLICANT: Kinney, Anthony J.
 ; APPLICANT: Rafalski, J. Antoni
 ; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
 ; FILE REFERENCE: BB-1178
 ; CURRENT APPLICATION NUMBER: US/09/364,230
 ; CURRENT FILING DATE: 1999-07-29
 ; EARLIER APPLICATION NUMBER: 60/094,990
 ; EARLIER FILING DATE: July 31, 1998
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 10
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-09-364-230-10

Query Match 5.6%; Score 161.5; DB 4; Length 234;
 Best Local Similarity 23.2%; Pred. No. 3e-07;
 Matches 49; Conservative 36; Mismatches 109; Indels 17; Gaps 4;

QY 358 VDMSTVDADTVTELAQVIVS-----RGGRF-----LEAPVSGNQOLSNDGMLVILAAGR 407
 DB 14 LDSSTIDPQTSRNLSTVTVNLRKKGDKWPKFLDAPVSGSVTAEEAGTLTFMVGSSE 73
 QY 408 GLYEDCSSCFQAMGKTSFPLGEVGNAAKMLIVNVQGSFMATIAEGLTLAHVTGSSQOT 467
 DB 74 EAFLAAPLLFSMGKSAIYCGGAGSGSAKICNNLALAVSMLGISEALALGOSLGVSAST 133
 QY 468 LLDILNQOLASIFLD--QKCNILQ-----GNFKPDEVLKYQKDLRLAIALGDAVNHP 520
 DB 134 LTNIENCSARCWSSDAYNPVFLMEGVPSFDYNGFGASKLMAKDNLNLAIVESAKLAGCK 193
 QY 521 TMAAAANEVYKRAKALQSDNDMSAVYRAY 551
 DB 194 YELTSQAQKIYTELCVSGHEAKDFSCAFPHY 224

RESULT 26
 US-09-788-657-22
 ; Sequence 22, Application US/09788657
 ; Patent No. 6656736
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas
 ; APPLICANT: Sassi, Philip
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Methods for generating hypermutable

[illegible]

Db 74 SI-----EEFVDSLEKPRILLVMKAGEA-TDKTIAALTPLHDKGILIDGG 119
Qy 380 GRFLEAPVSGNQQLSNDGMLV-----ILAAOGRLYEDCSCCFQAMGK 422
Db 120 NTFFKDTIRNRRELSAQGFNFIGTGVSGEGALKGPSIMPGQKEAYELVAPILEKTA 179
Qy 423 TS-----FFLGEVGNAAKMLIVNMVQGSFWATIAEGLT-LAHVTGQSQTLLDIL--- 472
Db 180 VADGEPCTYIGADGAGHYVQVHNGIEYQMDLIAEAYSVLKHSGLJTNELADTFTEW 239
Qy 473 NOGOLASIFLDOKONIL-----QGNFKDPFLYKIQKDLRLATLALGDAVNHPTPMAAAA 527
Db 240 NKGELSS-YLIEITADIFRKKDEGNLYVD-----VILDEANKGT----- 279
Qy 528 NEVYKRAKALQSDNDM-----SAYRAYI 552
Db 280 -----GKWTQSLLDLGVPVTLITESVFARYI 306

RESULT 29

US-09-252-991A-29147
; Sequence 29147, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29147
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29147

Query Match 4.8%; Score 138.5; DB 4; Length 316;
Best Local Similarity 24.3%; Pred. No. 8.1e-05;
Matches 44; Conservative 28; Mismatches 102; Indels 7; Gaps 2;
Qy 378 RGRFLEAPVSGNQQLSNDGMLVILAAAGDGLYEDCSCCFQAMGKTSFELGEVGNAAKMM 437
Db 130 RGLAMDAPVSGGTAGAAAGTLTFMVGGDAEALAKARPLFEAMGRNIFHAGDPDGAGQVAK 189
Qy 438 LIVNMVQGSFWATIAEGLTLAHVTGQSQTLLDILNQGLASIFLD--QKQNILQG--- 492
Db 190 VCNQQLAVLMTGTAEMALGVANGLEAKVLAEIMRSGGNWALEVYNPFWGVENAPA 249
Qy 493 --NFKPDPFLYKIQKDLRLATLALGDAVNHPTPMAAAANEVYKRAKALQSDNDMGAAYRA 550
Db 250 SRDVGSGFWAQLMAKDLGLAQBAAQASASTPMGSLALSLSYLLKLLKQGYAERDFSVQKL 309
Qy 551 Y 551
Db 310 F 310

RESULT 30

US-09-509-802-2
; Sequence 2, Application US/09509802
; Patent No. 6489130
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virga, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/09/509,802

; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-509-802-2
Query Match 4.7%; Score 135.5; DB 4; Length 786;
Best Local Similarity 20.0%; Pred. No. 0.0007;
Matches 126; Conservative 83; Mismatches 233; Indels 189; Gaps 30;
Qy 11 LVWKLGRYPWPWG-----KIVN-----PPKDLKKPRGKKCFVFKFFGTEDHAWI 55
Db 212 VIWGLVITQKPFADENKILHIMKVKVKGHRPELPP--ICRPRPRAC--ASLIGLMQRCWH 267
Qy 56 KVEQLKPYHAHKEMIKINKGRFQOAVDAVEFLRAKAGKDOTSSHNSDDKNRPNSE 115
Db 268 ADPQVRP-----TFQBITSETDLCEKPDREVVKDLAHEFGKSSLESKE 312
Qy 116 ERSRPNSGDEKR-----KLSLSEGVKVMKNMGEGK 144
Db 313 --ARPESRLRASAPPDNDCSLSSELLSOLDISQTLGPEELSRSSSECKLPSSSG 370
Qy 145 KRVS-----SGSSERGSKPLKRAEQSPKRGRPPKDKDLTIPESSTVKGMMAGPMA 198
Db 371 KRLSGVSSVDSAFSSRGSLS--LSPEREASTGDLG--PTD-----IQKKLVDAIISGDT 422
Qy 199 AFK--WQPTASEPVKADPHFHHLLSQTEKPAVCYQAITKKLICEETGTSITQAADS 256
Db 423 RLMKILQPDVDLVLDDSSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMA-- 480
Qy 257 TAVNGSIPTDKKIGFLGLGMLGSGIVSNLLKMGHTV-----TVNRTAEKCD--- 304
Db 481 -----VERK-----GRGIVELLARKTSVNAKDEQDWTALHFAQNGDEAST 522
Qy 305 -LFTIOEGARL-----GRTPAEVWSTCDITTFACVSDPKAAKDLV--LQPSGVYLGIRPK 355
Db 523 RLLLEKNASVNEVDPEGTPMHV-----AC---QHQQENIVRTLRRRGVDVGLQGD 571
Qy 356 CYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAAGDGLY----- 410
Db 572 AWLPLHYAAWQGHLPFIVKLLAKQPG-----VSVNAQ--TLDGRTPLHLAAQGRHYRVARI 624
Qy 411 -----EDCSSCFQAMGKTSFFLGEVGNAAKMMLI VNMVQGSFWATIAEGLTLAHVTGQSQ 465
Db 625 LIDLCSVDNICSLOQATPLHVAETGHTSTARLLHARGAGK--EALTSEGYTALHLAAQN- 682
Qy 466 QTLDLILNQGLASI--FLDQKQONILQGNFKPDPFLYKIQKDLRLATLALGDAVNHPTPM 523
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Qy 524 AAAANEVYKR---AKALQSDND--MSAYRA 550
Db 718 ----SEVVEELVSDALIDLSDPEQGLSALHLA 744

Search completed: September 16, 2004, 07:29:23
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:29:27 ; Search time 718 Seconds
(without alignments)

247.335 Million cell updates/sec

Title: US-10-067-482-2

Perfect score: 2866

Sequence:

1 MAAVSLRLGLVWGKLGKYP.....AKALDQSDNMSAVRAYIH 553

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 13423398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2866	100.0	553	US-10-067-482-2	Sequence 2, Appli
2	2811	98.1	547	US-10-067-482-3	Sequence 3, Appli
3	2798	97.6	550	US-10-103-313-417	Sequence 417, App
4	1410	49.2	276	US-10-067-482-4	Sequence 4, Appli
5	1404	49.0	269	US-10-103-313-540	Sequence 540, App
6	1291	45.0	249	US-09-987-755-2	Sequence 2, Appli
7	1291	45.0	260	US-10-103-313-474	Sequence 474, App
8	1286	44.9	250	US-10-103-313-317	Sequence 317, App
9	740.5	25.8	364	US-10-425-114-50561	Sequence 50561, A
10	727	25.4	293	US-10-437-963-174476	Sequence 174476,
11	720	25.1	290	US-10-167-547C-14	Sequence 14, Appl
12	695	24.2	289	US-10-167-547C-16	Sequence 16, Appl
13	682	23.8	333	US-10-424-599-144794	Sequence 144794,
14	569	19.9	343	US-10-437-963-116017	Sequence 116017,
15	567	19.8	256	US-10-425-114-42840	Sequence 42840, A

16	494.5	17.3	199	US-10-437-963-174477	Sequence 174477,
17	375	13.1	292	US-10-282-122A-52083	Sequence 52083, A
18	367	12.8	299	US-09-912-020-256	Sequence 256, App
19	354.5	12.4	344	US-10-767-701-42795	Sequence 42795, A
20	350	12.2	296	US-10-282-122A-56894	Sequence 56894, A
21	348.5	12.2	296	US-10-156-761-9081	Sequence 9081, Ap
22	347	12.1	344	US-10-437-963-151834	Sequence 151834,
23	340	11.9	295	US-10-282-122A-57891	Sequence 57891, A
24	334.5	11.7	295	US-10-123-965B-11	Sequence 11, Appl
25	331	11.5	286	US-10-282-122A-60763	Sequence 60763, A
26	331	11.5	305	US-10-156-761-9563	Sequence 9563, Ap
27	330	11.5	285	US-10-282-122A-59047	Sequence 59047, A
28	330	11.5	285	US-10-335-977-5655	Sequence 5655, Ap
29	327.5	11.4	290	US-10-282-122A-44990	Sequence 44990, A
30	324.5	11.3	288	US-10-282-122A-66301	Sequence 66301, A
31	318	11.1	296	US-10-282-122A-66289	Sequence 66289, A
32	314.5	11.0	277	US-10-282-122A-50872	Sequence 50872, A
33	314	11.0	297	US-10-282-122A-67475	Sequence 67475, A
34	313.5	10.9	301	US-10-282-122A-52906	Sequence 52906, A
35	305	10.6	350	US-10-424-599-255872	Sequence 255872, A
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37	301.5	10.5	292	US-10-287-274-438	Sequence 438, App
38	297.5	10.4	356	US-10-425-114-53506	Sequence 53506, A
39	296	10.3	176	US-10-767-701-60840	Sequence 60840, A
40	291.5	10.2	292	US-10-282-122A-74927	Sequence 74927, A
41	290.5	10.1	298	US-10-282-122A-61452	Sequence 61452, A
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43	282	9.8	318	US-10-282-122A-73480	Sequence 73480, A
44	281.5	9.8	291	US-10-424-599-255869	Sequence 255869,
45	281	9.8	291	US-10-282-122A-73480	Sequence 73480, A
46	281	9.8	336	US-10-043-487-224	Sequence 224, App
47	279.5	9.8	292	US-10-282-122A-75520	Sequence 75520, A
48	279.5	9.8	305	US-10-408-765A-755	Sequence 755, App
49	278	9.7	284	US-10-437-963-116817	Sequence 116817,
50	277	9.7	302	US-10-282-122A-49507	Sequence 49507, A
51	272.5	9.5	292	US-10-238-075-301	Sequence 301, App
52	272	9.5	288	US-10-282-122A-45255	Sequence 45255, A
53	269	9.4	297	US-10-282-122A-47679	Sequence 47679, A
54	256	8.9	121	US-10-767-701-60846	Sequence 60846, A
55	255	8.9	255	US-10-335-977-5654	Sequence 5654, Ap
56	254.5	8.9	552	US-10-437-963-114005	Sequence 114005,
57	229.5	8.0	1354	US-10-437-963-163633	Sequence 163633,
58	206.5	7.2	154	US-10-767-701-61555	Sequence 61555, A
59	205	7.2	81	US-10-767-701-52389	Sequence 52389, A
60	199.5	7.0	305	US-10-282-122A-51175	Sequence 51175, A
61	190.5	6.6	202	US-09-866-050A-651	Sequence 651, App
62	189	6.6	203	US-09-768-826-41	Sequence 41, Appl
63	189	6.6	203	US-09-833-245-2264	Sequence 2264, Ap
64	189	6.6	203	US-10-247-671-132	Sequence 132, App
65	187.5	6.5	274	US-10-425-114-69397	Sequence 69397, A
66	186.5	6.5	246	US-09-925-302-511	Sequence 511, App
67	186.5	6.5	246	US-09-925-302-511	Sequence 511, App
68	185.5	6.5	221	US-10-418-445-4	Sequence 4, Appli
69	185.5	6.5	237	US-09-938-885A-5	Sequence 5, Appli
70	185.5	6.5	240	US-09-938-885A-3	Sequence 3, Appli
71	185.5	6.5	240	US-09-987-755-7	Sequence 7, Appli
72	185.5	6.5	240	US-10-257-021-14	Sequence 14, Appl
73	185.5	6.5	240	US-10-207-791-2	Sequence 2, Appli
74	185.5	6.5	240	US-10-116-275-220	Sequence 220, App
75	185	6.5	240	US-10-424-599-243466	Sequence 243466,
76	181.5	6.3	305	US-10-156-761-8219	Sequence 8219, Ap
77	178.5	6.2	235	US-09-938-885A-1	Sequence 1, Appli
78	176	6.1	356	US-10-424-599-164051	Sequence 164051,
79	170.5	5.9	326	US-10-276-774-2486	Sequence 2486, Ap
80	169	5.9	314	US-09-768-826-43	Sequence 43, Appl
81	169	5.9	314	US-09-833-245-2266	Sequence 2266, Ap
82	169	5.9	670	US-09-823-187-86	Sequence 86, Appl
83	169	5.9	670	US-09-863-776-51	Sequence 51, Appl
84	169	5.9	671	US-09-946-374-308	Sequence 308, App
85	169	5.9	671	US-09-823-187-85	Sequence 85, Appl
86	169	5.9	671	US-09-863-776-20	Sequence 20, Appl
87	169	5.9	671	US-10-206-915-346	Sequence 346, App
88	169	5.9	671	US-10-199-670-346	Sequence 346, App

89 169 5.9 671 12 US-10-201-858-346 Sequence 346, App
90 169 5.9 671 12 US-10-205-890-346 Sequence 346, App
91 169 5.9 671 12 US-10-208-024-346 Sequence 346, App
92 169 5.9 671 12 US-10-201-853-346 Sequence 346, App
93 169 5.9 671 12 US-10-174-581-346 Sequence 346, App
94 169 5.9 671 12 US-10-176-483-346 Sequence 346, App
95 169 5.9 671 12 US-10-176-749-346 Sequence 346, App
96 169 5.9 671 12 US-10-176-914-346 Sequence 346, App
97 169 5.9 671 12 US-10-176-915-346 Sequence 346, App
98 169 5.9 671 12 US-10-006-485A-308 Sequence 308, App
99 169 5.9 671 12 US-10-013-907A-308 Sequence 308, App
100 169 5.9 671 12 US-10-015-499A-308 Sequence 308, App

ALIGNMENTS

RESULT 1
US-10-067-482-2
; Sequence 2, Application US/10067482
; Publication No. US20030148407A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc.
; TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
; FILE REFERENCE: 1U 102 R1
; CURRENT APPLICATION NUMBER: US/10/067,482
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-2

Query Match 100.0%; Score 2866; DB 14; Length 553;
Best Local Similarity 100.0%; Pred. No. 3e-235;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVSLRLGDLVWGKLGRIYPPWPGKI VNPDKLKKPRGKKCFVFFGTEHAWIKVEQL 60
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QY 61 KPYHAHKEEMIKINKGRFQQAVDAVEEFLRRAKGDQTSNNSDDKNRNSSEERSRP 120
DB 61 KPYHAHKEEMIKINKGRFQQAVDAVEEFLRRAKGDQTSNNSDDKNRNSSEERSRP 120
QY 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPKRAQEQSPRKRGRPPKDEK 180
DB 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPKRAQEQSPRKRGRPPKDEK 180
QY 181 LTIPESTVKGMMAGPMAAFKMQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK 240
DB 181 LTIPESTVKGMMAGPMAAFKMQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK 240
QY 241 ICEEETGTSIOAADSTAVNGSIPTDCKIGFLGLMGSGIVSNLLKMGHTVTVWNRTA 300
DB 241 ICEEETGTSIOAADSTAVNGSIPTDCKIGFLGLMGSGIVSNLLKMGHTVTVWNRTA 300
QY 301 EKCDLFIQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDM 360
DB 301 EKCDLFIQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDM 360
QY 361 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGRGLYEDCCSCFOAM 420
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QY 421 GKTSFELGVBGNAKKMMLIVNMVQGSFMATIAEGLTLAHTVGTOSQOTLLDILNQGLASI 480
DB 421 GKTSFELGVBGNAKKMMLIVNMVQGSFMATIAEGLTLAHTVGTOSQOTLLDILNQGLASI 480
QY 481 FLDDQKCNILQGNFKPDFYLYIKQDLRLAIALGDVAVNHPTMAAANEVYKRAKALDOS 540

DB 481 FLDDQKCNILQGNFKPDFYLYIKQDLRLAIALGDVAVNHPTMAAANEVYKRAKALDOS 540
QY 541 DNDSAVYRAYIH 553
DB 541 DNDSAVYRAYIH 553

ALIGNMENTS

RESULT 2
US-10-067-482-3
; Sequence 3, Application US/10067482
; Publication No. US20030148407A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc.
; TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
; FILE REFERENCE: 1U 102 R1
; CURRENT APPLICATION NUMBER: US/10/067,482
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 547
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-3

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Best Local Similarity 98.7%; Pred. No. 1.4e-230;
Matches 546; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
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DB 1 MAAVSLRLGDLVWGKLGRIYPPWPGKI VNPDKLKKPRGKKCFVFFGTEHAWIKVEQL 60
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DB 61 KPYHAHKEEMIKINKGRFQQAVDAVEEFLRRAKGDQTSNNSDDKNRNSSEERSRP 120
QY 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPKRAQEQSPRKRGRPPKDEK 180
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DB 241 ICEEETGTSIOAADSTAVNGSIPTDCKIGFLGLMGSGIVSNLLKMGHTVTVWNRTA 300
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DB 361 STVDADTVTELAAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAAGRGLYEDCCSCFOAM 420
QY 421 GKTSFELGVBGNAKKMMLIVNMVQGSFMATIAEGLTLAHTVGTOSQOTLLDILNQGLASI 480
DB 421 GKTSFELGVBGNAKKMMLIVNMVQGSFMATIAEGLTLAHTVGTOSQOTLLDILNQGLASI 480
QY 481 FLDDQKCNILQGNFKPDFYLYIKQDLRLAIALGDVAVNHPTMAAANEVYKRAKALDOS 540
DB 481 FLDDQKCNILQGNFKPDFYLYIKQDLRLAIALGDVAVNHPTMAAANEVYKRAKALDOS 540
QY 541 DNDSAVYRAYIH 553
DB 541 DNDSAVYRAYIH 547

RESULT 3
US-10-103-313-417
; Sequence 417, Application US/10103313

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; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 417
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-417

Query Match          97.6%; Score 2798; DB 14; Length 550;
Best Local Similarity 98.7%; Pred. No. 1.9e-229;
Matches 543; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 4 VSLRLGDLVWGKLGRIYPPWPKIVNPPKDLKKPRGKCFVKKPFGTGDHAWIKVEQLKPY 63
DB 7 VSLRLGDLVWGKLGRIYPPWPKIVNPPKDLKKPRGKCFVKKPFGTGDHAWIKVEQLKPY 66
QY 64 HAHKEEMIKINKGRFQQAQVDAVEEFLLRAKGDQTSNNSDDKNRNSSEERSRNSG 123
DB 67 HAHKEEMIKINKGRFQQAQVDAVEEFLLRAKGDQTSNNSDDKNRNSSEERSRNSG 126
QY 124 DEKRKLSLSEGVKKNMGEGKKRVSSGSSRGSKSPKRAEQSPKRGPPKDEKDLTI 183
DB 127 DEKRKLSLSEGVKKNMGEGKKRVSSGSSRGSKSPKRAEQSPKRGPPKDEKDLTI 186
QY 184 PESTVTKGMAGPMAAPKWOPTASEPVKADPHPHFLLSQTEKPAVCYQAITKKLICE 243
DB 187 PESTVTKGMAGPMAAPKWOPTASEPVKADPHPHFLLSQTEKPAVCYQAITKKLICE 246
QY 244 EETGSTSQAADSTAVNGSITPTDKTGFLGLGMLGSGIVSNLLKMGHTVTVMNRTEAKC 303
DB 247 EETGSTSQAADSTAVNGSITPTDKTGFLGLGMLGSGIVSNLLKMGHTVTVMNRTEAKC 305
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DB 306 -----EGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGSPGVLOGIRGKCYVDMSTV 360
QY 364 DADTVTELAQVIVSRGRGFLEAPVSGNQQLSDGMLVLAAGDRGLYEDCSSCFQAMGKT 423
DB 361 DADTVTELAQVIVSRGRGFLEAPVSGNQQLSDGMLVLAAGDRGLYEDCSSCFQAMGKT 420
QY 424 SFPLGEVGNAAKMWMLIVNVVQGSFMATIAEGLTLIAHVTGOSQOTLLDILNQGLASIFLD 483
DB 421 SFPLGEVGNAAKMWMLIVNVVQGSFMATIAEGLTLIAQVGTGOSQOTLLDILNQGLASIFLD 480
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DB 481 QKCNILQGNFKPDPFYLYIQKDLRLAIALGDVNHPTPMAAANAEVYKRAKALDQSDND 540
QY 544 MSAYVYRAYIH 553
DB 541 MSAYVYRAYIH 550

RESULT 4
US-10-067-482-4
; Sequence 4, Application US/10067482
; Publication No. US20030148407A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc.
; TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
; FILE REFERENCE: IU 102 R1
; CURRENT APPLICATION NUMBER: US/10/067,482
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4
; LENGTH: 276
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-4

Query Match          49.2%; Score 1410; DB 14; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGSIVSNLLKMGHTVTVMNRTEAKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAA 60
QY 338 KDLVLGSPGVLOGIRGKCYVDMSTVDADTVTELAQVIVSRGRGFLEAPVSGNQQLSDNG 397
DB 61 KDLVLGSPGVLOGIRGKCYVDMSTVDADTVTELAQVIVSRGRGFLEAPVSGNQQLSDNG 120
QY 398 MLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWMLIVNVVQGSFMATIAEGLTL 457
DB 121 MLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWMLIVNVVQGSFMATIAEGLTL 180
QY 458 AHVTGOSQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFYLYIQKDLRLAIALGDV 517
DB 181 AHVTGOSQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFYLYIQKDLRLAIALGDV 240
QY 518 NHPTPMAAANAEVYKRAKALDQSDNDMSAVYRAYIH 553
DB 241 NHPTPMAAANAEVYKRAKALDQSDNDMSAVYRAYIH 276

RESULT 5
US-10-103-313-540
; Sequence 540, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 540
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (4)_feature
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (165)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-540

Query Match          49.0%; Score 1404; DB 14; Length 269;
Best Local Similarity 99.3%; Pred. No. 4.5e-111;
Matches 267; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VSLRLGDLVWGKLGRIYPPWPKIVNPPKDLKKPRGKCFVKKPFGTGDHAWIKVEQLKPY 63
DB 1 VSLRLGDLVWGKLGRIYPPWPKIVNPPKDLKKPRGKCFVKKPFGTGDHAWIKVEQLKPY 60
QY 64 HAHKEEMIKINKGRFQQAQVDAVEEFLLRAKGDQTSNNSDDKNRNSSEERSRNSG 123
DB 61 HAHKEEMIKINKGRFQQAQVDAVEEFLLRAKGDQTSNNSDDKNRNSSEERSRNSG 120
QY 124 DEKRKLSLSEGVKKNMGEGKKRVSSGSSRGSKSPKRAEQSPKRGPPKDEKDLTI 183
DB 121 DEKRKLSLSEGVKKNMGEGKKRVSSGSSRGSKSPKRAEQSPKRGPPKDEKDLTI 180
```

QY 184 PESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLKICE 243
Db 181 PESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLKICE 240
QY 244 BETGSTSQAADSTAVNGSIPTDKKIGF 272
Db 241 BETGSTSQAADSTAVNGSIPTDKKIGF 269

RESULT 6

US-09-987-755-2
; Sequence 2, Application US/09987755
; Publication No. US20030022312A1
; GENERAL INFORMATION:
; APPLICANT: Kunsch et al
; TITLE OF INVENTION: Human Hepatoma-Derived Growth Factor-2
; FILE REFERENCE: PF198D1C1
; CURRENT APPLICATION NUMBER: US/09/987,755
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 09/263,625
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 08/464,600
; PRIOR FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: human
US-09-987-755-2

Query Match 45.0%; Score 1291; DB 10; Length 249;
Best Local Similarity 99.6%; Pred. No. 1.7e-101;
Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQL 60
Db 1 MAAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQL 60
QY 61 KPYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 120
Db 61 KPYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 120
QY 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 180
Db 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 180
QY 181 LTIPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLK 240
Db 181 LTIPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLK 240
QY 241 ICEE 244
Db 241 ICED 244

RESULT 7

US-10-103-313-474
; Sequence 474, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 474
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-103-313-474

Query Match 45.0%; Score 1291; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-101;
Matches 243; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQL 60
Db 12 MAAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQL 71
QY 61 KPYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 120
Db 72 KPYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 131
QY 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 180
Db 132 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 191
QY 181 LTIPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLK 240
Db 192 LTIPESSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKKLK 251
QY 241 ICEE 244
Db 252 ICED 255

RESULT 8

US-10-103-313-317
; Sequence 317, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 317
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-317

Query Match 44.9%; Score 1286; DB 14; Length 250;
Best Local Similarity 99.6%; Pred. No. 4.6e-101;
Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQLK 61
Db 3 AAVSLRLGDLVWGKLGRIYPPWPGKIVNPPKDLKKPRGKCCFFVKFFGTEDHAWIKVEQLK 62
QY 62 PYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 121
Db 63 PYHAHKEEMIKINKGRFQQAQVDAVEEFLRAKGDQTSNHNSSDDKNRRNSSEERSRP 122
QY 122 SGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 181
Db 123 SGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKPLKRAQOSPRKGRPPKDEKD 182
QY 182 TIPESSSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKLKI 241
Db 183 TIPESSSTVKGMMAGPMAAFKQPTASEPVKADDPHFHFLLSQTEKPAVCYQAITTKLKI 242
QY 242 CEE 244
Db 243 CED 245

RESULT 9

US-10-425-114-50561


```

; Sequence 50561, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 50561
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pap
; US-10-425-114-50561

Query Match      25.8%; Score 740.5; DB 12; Length 364;
Best Local Similarity 47.8%; Pred. No. 2.6e-54;
Matches 160; Conservative 54; Mismatches 104; Indels 17; Gaps 5;

Qy 216 HFHFLLSQTKP-AVCYQAITKK-LKICEETGTSIQAADSTAVNGSIPTDKKIGFL 273
Db 31 HKH---TRTQPSAYTREGTRSNVACAE-----GTEEG-CQOSEMEVGFL 75

Qy 274 GLGLMGSGIVNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVVTCTDITPACVSD 333
Db 76 GLGIMGKAMATNLLRHGFRVTVMNRTLAKCQELVALGATVGETPASVVKCRYIIMLSD 135

Qy 334 PKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNOQL 393
Db 136 PSAALSVPFDKGVLEQIGSGKGYVDMSTVDAATSTKISEAVKQKGAFLEAPVSGSKPP 195

Qy 394 SNGQMLVILAAGDRGLYEDCSSCFQAMGKTSFFELGEGVNAAKMMLIVNMVQGSFWATIAE 453
Db 196 AEDQVILAAGDRPLVDGMPAPFDVLGKGSFFELGEGVNAAKMMLIVNMVQGSFWATIAE 255

Qy 454 GLTIAHVTGSGQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFLKYIOKDLRLAIAL 513
Db 256 GLCLADKSLGSPQTLDDVLDLGAIANPMPFKLGPSMLQGSYNPAFLPKHQQKDMRLAIAL 315

Qy 514 GDVAVNHTPMAAANAEVYKRAKALDOSDNDMSAVY 548
Db 316 GDENAVAMPVSAANAEAFKARSGLGLGDFSAVY 350

RESULT 10
US-10-437-963-174476
; Sequence 174476, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174476
; LENGTH: 293

; Sequence 50561, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 50561
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pap
; US-10-425-114-50561

Query Match      25.8%; Score 740.5; DB 12; Length 364;
Best Local Similarity 47.8%; Pred. No. 2.6e-54;
Matches 160; Conservative 54; Mismatches 104; Indels 17; Gaps 5;

Qy 216 HFHFLLSQTKP-AVCYQAITKK-LKICEETGTSIQAADSTAVNGSIPTDKKIGFL 273
Db 31 HKH---TRTQPSAYTREGTRSNVACAE-----GTEEG-CQOSEMEVGFL 75

Qy 274 GLGLMGSGIVNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVVTCTDITPACVSD 333
Db 76 GLGIMGKAMATNLLRHGFRVTVMNRTLAKCQELVALGATVGETPASVVKCRYIIMLSD 135

Qy 334 PKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNOQL 393
Db 136 PSAALSVPFDKGVLEQIGSGKGYVDMSTVDAATSTKISEAVKQKGAFLEAPVSGSKPP 195

Qy 394 SNGQMLVILAAGDRGLYEDCSSCFQAMGKTSFFELGEGVNAAKMMLIVNMVQGSFWATIAE 453
Db 196 AEDQVILAAGDRPLVDGMPAPFDVLGKGSFFELGEGVNAAKMMLIVNMVQGSFWATIAE 255

Qy 454 GLTIAHVTGSGQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFLKYIOKDLRLAIAL 513
Db 256 GLCLADKSLGSPQTLDDVLDLGAIANPMPFKLGPSMLQGSYNPAFLPKHQQKDMRLAIAL 315

Qy 514 GDVAVNHTPMAAANAEVYKRAKALDOSDNDMSAVY 548
Db 316 GDENAVAMPVSAANAEAFKARSGLGLGDFSAVY 350

RESULT 11
US-10-167-547C-14
; Sequence 14, Application US/10167547C
; Publication No. US20030170653A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company
; APPLICANT: Damude, Howard G.
; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
; TITLE OF INVENTION: Butyrolactone and its Intermediates
; FILE REFERENCE: CL1804 US NA
; CURRENT APPLICATION NUMBER: US/10/167,547C
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/297198
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Microsoft Office 07
; SEQ ID NO 14
; LENGTH: 290
; TYPE: PRT
; ORGANISM: tulip pistil
; US-10-167-547C-14

Query Match      25.1%; Score 720; DB 14; Length 290;
Best Local Similarity 50.7%; Pred. No. 1e-52;
Matches 142; Conservative 52; Mismatches 86; Indels 0; Gaps 0;

Qy 269 KIGFLGLMGSGIVNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVVTCTDITF 328
Db 2 EVGFLGLGIMGKAMAVNLLRSGFRVTVMNRTLSKCNELLEQSGASVGETPAAVVKCKYTI 61

Qy 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
Db 62 AMLSDPSAALSVPFDKGVLEQIGSGKGYVDMSTVDAATSTKISEAITQKGHFLEAPVS 121

Qy 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFELGEGVNAAKMMLIVNMVQGSFM 448
Db 122 GSKKPAEDGQVLVILAAGDKVLYDDMVPAFDVLGKGSFFELGEGVNAAKMMLIVNMVQGSFM 181

Qy 449 ATIAEGLTLAHVTGSGQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFLKYIOKDLR 508
Db 182 NALSEGLSLAGSKGLEQTKLLDVLDLGAIANPMPFKLGPSMLQGSYNPAFLPKHQQKDMR 241

; Sequence 174476, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174476
; LENGTH: 293

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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72412C.1.pap
; US-10-437-963-174476

Query Match      25.4%; Score 727; DB 16; Length 293;
Best Local Similarity 52.1%; Pred. No. 2.7e-53;
Matches 146; Conservative 49; Mismatches 85; Indels 0; Gaps 0;

Qy 269 KIGFLGLMGSGIVNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVVTCTDITF 328
Db 2 EVGFLGLGIMGKAMAVNLLRSGFRVTVMNRTLSKCNELLEQSGASVGETPAAVVKCKYTI 61

Qy 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
Db 62 AMLSDPSAALSVPFDKGVLEQIGSGKGYVDMSTVDAATSTKISEAITQKGHFLEAPVS 121

Qy 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFELGEGVNAAKMMLIVNMVQGSFM 448
Db 122 GSKKPAEDGQVLVILAAGDKVLYDDMVPAFDVLGKGSFFELGEGVNAAKMMLIVNMVQGSFM 181

Qy 449 ATIAEGLTLAHVTGSGQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFLKYIOKDLR 508
Db 182 NALSEGLSLADNSGLSPQTLDDVLDLGAIANPMPFKLGPSMLQGSYNPAFLPKHQQKDMR 241

Qy 509 LAIALGDVAVNHTPMAAANAEVYKRAKALDOSDNDMSAVY 548
Db 242 LALALGDENAVMPVAAASNEAFKARSGLGLGDFSAVY 281

RESULT 11
US-10-167-547C-14
; Sequence 14, Application US/10167547C
; Publication No. US20030170653A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company
; APPLICANT: Damude, Howard G.
; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
; TITLE OF INVENTION: Butyrolactone and its Intermediates
; FILE REFERENCE: CL1804 US NA
; CURRENT APPLICATION NUMBER: US/10/167,547C
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/297198
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Microsoft Office 07
; SEQ ID NO 14
; LENGTH: 290
; TYPE: PRT
; ORGANISM: tulip pistil
; US-10-167-547C-14

Query Match      25.1%; Score 720; DB 14; Length 290;
Best Local Similarity 50.7%; Pred. No. 1e-52;
Matches 142; Conservative 52; Mismatches 86; Indels 0; Gaps 0;

Qy 269 KIGFLGLMGSGIVNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVVTCTDITF 328
Db 2 EVGFLGLGIMGKAMAVNLLRSGFRVTVMNRTLSKCNELLEQSGASVGETPAAVVKCKYTI 61

Qy 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
Db 62 AMLSDPSAALSVPFDKGVLEQIGSGKGYVDMSTVDAATSTKISEAITQKGHFLEAPVS 121

Qy 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFELGEGVNAAKMMLIVNMVQGSFM 448
Db 122 GSKKPAEDGQVLVILAAGEKALYEIIPAFELVGLGKGSFFELGEGVNAAKMMLIVNMVQGSFM 181

Qy 449 ATIAEGLTLAHVTGSGQOTLLDILNQGLASIFLDQKCNILQGNFKPDPFLKYIOKDLR 508
Db 182 NALSEGLSLAGSKGLEQTKLLDVLDLGAIANPMPFKLGPSMLQGSYNPAFLPKHQQKDMR 241

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QY 482 LDQKCONILGNFKPDFYIKYIQDLRLAIALGDAVNHPPTMAAAANEVYKRAKALDQSD 541
Db 267 FSLKGPSVMVKAAYPTAPFLKHQQDLRLAALAESVSQSITVAANAELYKVAKSLGLAD 326
QY 542 NDMSAVYRA 550
Db 327 QDPSAVIEA 335

RESULT 15
US-10-425-114-42840
; Sequence 42840, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42840
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700580946_FLI.pep
US-10-425-114-42840

Query Match 19.8%; Score 567; DB 12; Length 256;
Best Local Similarity 46.1%; Pred. No. 9.6e-40;
Matches 111; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 310 GARLGRTPAEVSTCDITFACVSDPKAAKDLVLGSPGVLOGIRPKCYVDVMTDADTVT 369
Db 5 GAKYEPTPAQVASCVDVTFAMLADPQSAAEVACCGSAGLAPGKGYVDVSTVDGATSK 64
QY 370 ELAQVIVSRGRFLEAPVSGNQSLNDGMLVILAAAGDRGLYEDCSCFCQAMGKTSFFLGE 429
Db 65 LIGERITSTGASFLAPVSGSKPAEDGLIFLTAGDESLYKRVAPLLDVMGKSRFLGD 124
QY 430 VGNAAKMMLVNMVQGSFMATIAEGLTLAHVTGQSQOTLLDILNQGLASIFLDQKQNI 489
Db 125 VGNGAAMKLVNMVQGSFMVVSFSEGLLSKVKGLDPTNLVEVISQGAISAPMFSLKGPSM 184
QY 490 LQGNFKPDFYIKYIQDLRLAIALGDAVNHPPTMAAAANEVYKRAKALDQSDNDMSAVYR 549
Db 185 VKAAYPPAPFLKHQQDLRLAALAESVSQSITVAANAELYKRAKSLGSDHDFSAVIE 244
QY 550 A 550
Db 245 A 245

RESULT 16
US-10-437-963-174477
; Sequence 174477, Application US/10437963
; Publication No. US20040123342A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174477
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(199)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72413C.1.pep
US-10-437-963-174477

Query Match 17.3%; Score 494.5; DB 16; Length 199;
Best Local Similarity 52.3%; Pred. No. 9.9e-34;
Matches 101; Conservative 31; Mismatches 60; Indels 1; Gaps 1;

QY 287 LKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVYVSTCDITFACVSDPKAAKDLVLGSPG 346
Db 1 LRHGRFVTVNRTLSKQELVALGAAVGETPAAVAKCRVTIAMLSDPSSAALSVPFDKDG 60
QY 347 VLOGIRPKCYVDVMTDADTVTTELAQVIVSRGRFLEAPVSGNQSLNDGMLVILAAAG 406
Db 61 VLEQIGEGKGYVDVMTDADTSCISKISAIKQKGAFVEAPVSGSKPAEDGQLVILAAAG 120
QY 407 RGLYEDCSCFCQAMGKTSFFLGEVGNAAKMWMLVNMVQGSFMATIAEGLTLAHVTGQSQQ 466
Db 121 KVLVDDMVPAFDVLGKKSFFLGEIGNGAKMKLVNMVIXG-MNNAISEGLSLADNSGLSPQ 179
QY 467 TLDILNQGLAS 479
Db 180 TLFVDLDLGAIAN 192

RESULT 17
US-10-282-122A-52083
; Sequence 52083, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
```

Query Match 12.8%; Score 367; DB 9; Length 299;
Best Local Similarity 29.4%; Pred. No. 1.4e-22;

```

; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56894
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-56894

Query Match          12.2%; Score 350; DB 12; Length 296;
Best Local Similarity 29.9%; Pred. No. 3.8e-21;
Matches      79; Conservative 49; Mismatches 136; Indels 0; Gaps 0

QY    269   KIGFLGGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVWSTCDITF 328
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    3     KIGFIGTGVWGKSIIRNMKNLSVNYNRTKSTDDLVABEAVWYDTPKAIAEASDIIF 62

QY    329   ACVSDPKAAKDVLPGSGVIQGIRPGKYVDIMSTVDADTVELAQVIVSRGRFLEAPVS 388
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    63     TMVGFFSDVEGVYFNETGIQADLTGKIWDLTSTPTLAEKIAKKAAEVGAHALDAPVS 122

QY    389   GNQLSNDGMVLILAGDRGLYEDCCSCFOAMGKTSPFLGEVGNAAKMMLIVNNMVQGSFM 448
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    123    GGDLGAKNGTLTIMVGGDQESYDTPLVPFTFKTGTFMLHGSAGKGQHTKMANQLMIAGTM 182

QY    449   ATTAEGTLTAHVTSQSOTLLDILNQLASIFIIDQKCONILQGNFKPFDVLVKYIQDKLR 508
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    183    TGITEMLVYANATGLTEKLEVTVGGSSAANWSLSNYGPRIKKBDYTPGFVFVKFIKDLR 242

QY    509   LAIALGDVANHPTPTMAAAANEVYK 532
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    243    IALDEAKKLDPLPATQKATELYE 266

RESULT 21

```

```
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51941C.1.1.pap
US-10-437-963-151834

Query Match      12.1%; Score 347; DB 16; Length 344;
Best Local Similarity 27.5%; Pred. No. 8.6e-21;
Matches 84; Conservative 65; Mismatches 149; Indels 8; Gaps 4;

QY 233 QAITKK---LKICEETSTSIQAADSTAVNGS----IPTDKKIGFLGLMGSGIVSNL 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 RSLTRRRPPLPSAAAAAAMSSATGVNVSDFPISPDITTRVAVVGTGVNGSQMAGHL 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 287 LKMGHTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLP 345
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 LAAGYALVTVNRTASAKGLVSRGATLAESPRAAAAAADVIFLMVGFSDVRSTSLDPST 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 GVLQIRPKCKVDMSTVDADTVTTELAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAG 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 GALAGLAPGGLLVDMTSDPTLAEIAEAAAASCAAVDAPVSGDGRGARSATLSIFAGG 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 406 DRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIUNMVQGSFMAIEGLTLAHVTGSSQ 465
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 DAAVVARLAPLPLKMG-NALYMGPGAGQRAKLGNAIAASTMVGLVEGMVYAHKAGLDV 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 466 QTLIDLINQQLASIFLDQKCNILQGNFKPDPFLYLYKIQKDLRLALALGDVAVNHPTMAA 525
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 AKWLEAISTGAAGSKSLDLYGRMLERDMAAGFYVRHFVKDLGICLISECQAMGLALPGLA 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 526 AANEVY 531
      : : : : :
Db 306 LAHQLY 311
      : : : : :

RESULT 23
US-10-282-122A-57891
; Sequence 57891, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09

; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51941C.1.1.pap
US-10-437-963-151834

Query Match      12.1%; Score 347; DB 16; Length 344;
Best Local Similarity 27.5%; Pred. No. 8.6e-21;
Matches 84; Conservative 65; Mismatches 149; Indels 8; Gaps 4;

QY 233 QAITKK---LKICEETSTSIQAADSTAVNGS----IPTDKKIGFLGLMGSGIVSNL 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 RSLTRRRPPLPSAAAAAAMSSATGVNVSDFPISPDITTRVAVVGTGVNGSQMAGHL 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 287 LKMGHTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLP 345
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 LAAGYALVTVNRTASAKGLVSRGATLAESPRAAAAAADVIFLMVGFSDVRSTSLDPST 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 GVLQIRPKCKVDMSTVDADTVTTELAQVIVSRGRFLEAPVSGNQQLSNDGMLVILAAG 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 GALAGLAPGGLLVDMTSDPTLAEIAEAAAASCAAVDAPVSGDGRGARSATLSIFAGG 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 406 DRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIUNMVQGSFMAIEGLTLAHVTGSSQ 465
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 DAAVVARLAPLPLKMG-NALYMGPGAGQRAKLGNAIAASTMVGLVEGMVYAHKAGLDV 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 466 QTLIDLINQQLASIFLDQKCNILQGNFKPDPFLYLYKIQKDLRLALALGDVAVNHPTMAA 525
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 AKWLEAISTGAAGSKSLDLYGRMLERDMAAGFYVRHFVKDLGICLISECQAMGLALPGLA 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 526 AANEVY 531
      : : : : :
Db 306 LAHQLY 311
      : : : : :

RESULT 23
US-10-282-122A-57891
; Sequence 57891, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09

; ORGANISM: Enterococcus faecium
US-10-282-122A-57891

Query Match      11.9%; Score 340; DB 12; Length 295;
Best Local Similarity 28.8%; Pred. No. 2.7e-20;
Matches 76; Conservative 52; Mismatches 136; Indels 0; Gaps 0;

QY 269 KIGFLGLMGSGIVSNLLKMGHTTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 KLGFIGTGVMSGSAVARHLEAGHEAVTVNRTAKADPLVTEGAIWADTFKAVAESNLIF 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 329 ACVSDPKAAKDLVLGPGSVLQGIREFKCYKCYDMSTVDADTVTTELAQVIVSRGRFLEAPVS 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TMVGYPKDVEEIIYQSGIFSADISGHILVDLTSTPSLAEKIAKTAKEKGADALDAPVS 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIUNMVQGSFM 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 GGDLAGKNGTTLTMVGGBEAVVDVLPFKFEGTFTTLHGSAGKGQHTKVAQNIIMAGTM 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 ATIAEGLTLAHVTGSSQQTLLDLINQQLASIFLDQKCNILQGNFKPDPFLYLYKIQKDLR 508
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 TGTEMLVYAKNGLDLKKVITLTLSSGSAANWSLSNYSRILKEDYTFGFFVHKFIKDLK 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 LAIALGDVAVNHPTPMAAAANEVYK 532
      : : : : :
Db 242 IALEEAEKMDLVLPATTQALKLYE 265
      : : : : :

RESULT 24
US-10-123-965B-11
; Sequence 11, Application US/10123965B
; Publication No. US20030099966A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Sheng-He
; TITLE OF INVENTION: E. Coli Virulence Determinants and Methods of Use Thereof
; FILE REFERENCE: US/1841A-SHH
; CURRENT APPLICATION NUMBER: US/10/123,965B
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/284,762
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-123-965B-11

Query Match      11.7%; Score 334.5; DB 14; Length 295;
Best Local Similarity 28.7%; Pred. No. 7.9e-20;
Matches 81; Conservative 53; Mismatches 147; Indels 1; Gaps 1;

QY 270 IGFLGLMGSGIVSNLLKMGHTTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDITFA 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 IGFIGTGMKPMAYNLOQAGHTLYFSAHFEPAPQEFIGERGIVCSTPTEVAQCEVIIT 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 CVSDPKAAKDLVLGPGS-GVLOGIRPGKCVDMSTVDADTVTTELAQVIVSRGRFLEAPVS 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 MLPDTPHVEDVLPHFNYPVGHLSHGKIVIDMSSISPVATKAFQAQLIAVGAVIDAPVS 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIUNMVQGSFM 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 GGEVGAKAGTSLSIMVGGCEVYLIQKPILELMGKNITLVGNVGGTGTCKVANOIIVALNI 182
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 ATIAEGLTLAHVTGSSQQTLLDLINQQLASIFLDQKCNILQGNFKPDPFLYLYKIQKDLR 508
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; ORGANISM: Enterococcus faecium
US-10-282-122A-57891

Query Match      11.9%; Score 340; DB 12; Length 295;
Best Local Similarity 28.8%; Pred. No. 2.7e-20;
Matches 76; Conservative 52; Mismatches 136; Indels 0; Gaps 0;

QY 269 KIGFLGLMGSGIVSNLLKMGHTTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 KLGFIGTGVMSGSAVARHLEAGHEAVTVNRTAKADPLVTEGAIWADTFKAVAESNLIF 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 329 ACVSDPKAAKDLVLGPGSVLQGIREFKCYKCYDMSTVDADTVTTELAQVIVSRGRFLEAPVS 388
      : : : : ~ : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TMVGYPKDVEEIIYQSGIFSADISGHILVDLTSTPSLAEKIAKTAKEKGADALDAPVS 121
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
QY 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIUNMVQGSFM 448
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
Db 122 GGDLAGKNGTTLTMVGGBEAVVDVLPFKFEGTFTTLHGSAGKGQHTKVAQNIIMAGTM 181
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
QY 449 ATIAEGLTLAHVTGSSQQTLLDLINQQLASIFLDQKCNILQGNFKPDPFLYLYKIQKDLR 508
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
Db 182 TGTEMLVYAKNGLDLKKVITLTLSSGSAANWSLSNYSRILKEDYTFGFFVHKFIKDLK 241
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
QY 509 LAIALGDVAVNHPTPMAAAANEVYK 532
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
Db 242 IALEEAEKMDLVLPATTQALKLYE 265
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : :
```

Db 183 EAVAEALLFASKSGADPARVREALMGGLASSRVLEVHGERMIKGTFFPGFRISAHQDLN 242
 QY 509 LAIALGDVAVNHPTMAAAANEVYKRAKALDQSDNDMSAVYRA 550
 Db 243 LALENARLLNTPLENTATTOQLFSACAALGGKWDHLSALIRA 284

RESULT 25

US-10-282-122A-60763
 ; Sequence 60763, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA 034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 60763
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Listeria monocytogenes
 US-10-282-122A-60763

Query Match 11.5%; Score 331; DB 12; Length 286;
 Best Local Similarity 27.1%; Pred. No. 1.5e-19;
 Matches 77; Conservative 59; Mismatches 148; Indels 0; Gaps 0;
 QY 268 KKIGFLGLMGSGIVSNLLKMGHTVTWNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
 Db 2 EKIGFVGTGVMGSSMAGHLLBAGYELVYTKTKAEDLLDKGALWVETPGELANKVDIL 61
 QY 328 FACVSDPKAAKDLVLGPGSVLQGRPGKYVDMSTVDADTVTELAQVTVSRGGRFLEAPV 387
 Db 62 ISMVGYPKDVLELYGNGFLENLAAGTVADMTTSSPALAKKWAEBRGREGIGVLDAPV 121
 QY 388 SGNQOLNDGMLVILAAAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAKMMILVNMVQGSF 447
 Db 122 SGGDIGAKNGTSLSMWGSSEBDFLKVKPIFDILGSSVILQDAGAGQHTKWNQIATSN 181

QY 448 MATIAGLTTLAHVTGQSQOTLLDILNOGLASIFLDQCKQNIQGNFKPDEVLKYIQKDL 507
 Db 182 MIGVTEAIIYAEAAAGLPSRVLDISGGAAGSWSLANLIPRVLKDDFSPGFIFKFIKDM 241
 QY 508 RLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDNDMSAVYRA 551
 Db 242 GIAISEAKQMGLELPLGLTLAEKMYQTLAEQGLSEEGTOALIKYY 285

RESULT 26

US-10-156-761-9563
 ; Sequence 9563, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 9563
 ; LENGTH: 305
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-9563

Query Match 11.5%; Score 331; DB 14; Length 305;
 Best Local Similarity 27.5%; Pred. No. 1.7e-19;
 Matches 80; Conservative 55; Mismatches 146; Indels 10; Gaps 2;
 QY 265 PTDKKIGFLGLMGSGIVSNLLKMGHTVTWNRTAEKCDLFIQEGARLGRTPAEVSTC 324
 Db 11 PARLVAVWIGLIGMSPMSNLKAGYDVTGFTLEQDKLDELTAAGTAAGSIAEAVRDA 70
 QY 325 DITFACVSDPKAAKDLVLGPGSVLQGRPGKYVDMSTVDADTVTELAQVTVSRGGRFLE 384
 Db 71 DVVITMVPASQVEAISYGPDLLENARSGALLIDMSITPRTSVDLAEAAAAGIRVLD 130
 QY 385 APVSGNQLNDGMLVILAAAGDRGLYEDCSCFOAMGKTSFFLGEVG-----NAKMWLI 439
 Db 131 APVSGGAGAVEAVLSIMVGGQADFEAKPVFEALGRTIVLCGPHGAGQTVKAAQNLIV 190
 QY 440 VNMVQGSFMATIAEGLTLAHVTGQSQOTLLDILNOGLASIFLDQCKQNIQGNFKPDPY 499
 Db 191 AVNIQ-----ACAEAVVFLKSGVDLKAALDVLGGGLAGSTVLRKKNFLHRPFKCFR 245
 QY 500 LKTYQKDLRLAIALGDVAVNHPTMAAAANEVYKRAKALDQSDNDMSAVYRA 550
 Db 246 IDLHHKDMGIVTDAARAAGVGAALPVGAVALVAALRAQGGDLHLSALLRS 296

RESULT 27

US-10-282-122A-59047
 ; Sequence 59047, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith

```

; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59047
; LENGTH: 285
; TYPE: prt
; ORGANISM: Helicobacter pylori
; US-10-282-122A-59047

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Query Match	11.5%;	Score 330;	DB 12;	Length 285;
Best Local Similarity	32.7%;	Pred. No. 1.8e-13;		
Matches	92;	Conservative 46;	Mismatches 137;	Indels 6; Gaps 4;
QY	269	KIGFLGGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEWSCTDITF	328	
Db	2	KIGWIGLGAGCTPMATRLRDAGLEVSVNRTESKAAPLKEKGVAVYTSPIDLAAKVDLVF	61	
QY	329	ACTVSDPKAAKDLVLPGSGVLGIGIRPGKCYVDMSTVDATVETLAAQIVVSRGRLEAPVS	388	
Db	62	TMLUSD-KAAADAVLAPKFWEQMSK-KIVVMNSTIAPLESLSBKIAQKHQATYLEAPVS	118	
QY	389	GNQQLSNDGMELVILAAAGDRGLYEDCSFCQAMGKTSFPLGEVGNAAKMVLIVNNVQGSFM	448	
Db	119	GSVCAAKAGALLILAAAGDEEIVSKLPVLAHLGSGQTFVLGKVGQGTGAKLSINSLLAQMG	178	
QY	449	ATIAEGLTIAHVTQSQOQTLLDILNOGLASIFLDQKCNITLOGNFXPDFVLKVIQKDLR	508	
Db	179	VAYSEALLKRLGVDAEASFLOIIGQSGMNSPLFOAKKGMWLQDNYPAAFSLKLMKADIR	238	
QY	509	LA-IALGDVANHPTFMAAAANEVYKRAKALDQSDNDMSAVY	548	
Db	239	LAKNEAFEMK--LPTFLFOAEELYSQAEKSGSLGGLDMAAVY	277	

RESULT 28
US-10-335-977-5655
; Sequence 5655, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS

```

1 NUMBER OF SEQUENCES: 10031
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: LAHIVE & COCKFIELD
4 STREET: 28 State Street
5 CITY: Boston
6 STATE: Massachusetts
7 COUNTRY: USA
8 ZIP: 02109-1875
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: CD/ROM ISO9660
11 COMPUTER: IBM PC Compatible
12 OPERATING SYSTEM: Windows NT 4.0
13 SOFTWARE: UNIX
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/10/335,977
16 FILING DATE: 30-Dec-2002
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/993,002
19 FILING DATE: 17-DEC-1997
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Mandragouras, Amy E.
22 REGISTRATION NUMBER: 36,207
23 REFERENCE/DOCKET NUMBER: GTN-018
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (617) 227-7400
26 TELEFAX: (617) 742-4214
27 INFORMATION FOR SEQ ID NO: 5655:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 285 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 HYPOTHETICAL: YES
34 ORIGINAL SOURCE:
35 ORGANISM: Helicobacter pylori
36 FEATURE:
37 NAME/KEY: misc feature
38 LOCATION: (B) LOCATION 1...285
39 SEQUENCE DESCRIPTION: SEQ ID NO: 5655:
40 US-10-335-977-5655

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Query Match	11.5%;	Score 330;	DB 12;	Length 285;
Best Local Similarity	32.7%;	Pred. No. 1.8e-19;		
Matches	92;	Conservative 46;	Mismatches 137;	Indels 6; Gaps 4
Qy	269	KIGFLGLMGSGIVSNLLKMGHTVWNNRTAEKCDLFIORGARLGRTPAEWSTCDITF	328	
Db	2	KIGWIGLGAMGTPWATLRDAGLEVSVYNRTESKAAPLKEKGVAVYTSPIDLAAKVDLVF	61	
Qy	329	ACVSDPKAAKDXLVLPSPGVLOGTRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS	388	
Db	62	TMLSD-KAAITDAVLAPKFWEQMSK-KIVVNMSTIAPLESLSLEKIAQKHQATYLEAPVS	118	
Qy	389	GNQQLSNDGMVLIIAAGDRGLYEDSCSPQAMGKTSFELGEVGNAAKMLIVNNVQGSFM	448	
Db	119	GSVCAAKAGALLIIAAGDEEIVSKLPEVLAHLSGQTFVLGKVGQGTGAKLSINSLLAQMG	178	
Qy	449	ATTABGLTLAHVTGQSQOITLIDILNQQLASIFLDQKQNILQGNFPDFVLKVIQKDLR	508	
Db	179	VAYSEALLAKRLGVDAESFLQIIGSGMNSPLFOAKKGMWLQNYPAAFSLKLMKXDIR	238	
Qy	509	LA-IALGDVANNHPTPMAAAANEVYKRAKALDQSDNDMSAVY	548	
Db	219	LAKNEAGEAMK-LPFLFOAEELLYSOAEKSLGSLGLDMAAVY	277	

RESULT 29

US-10-282-122A-44990

; Sequence 44990, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 44990

; LENGTH: 290

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-10-282-122A-44990

Query Match 11.4%; Score 327.5; DB 12; Length 290;

Best Local Similarity 27.8%; Pred No. 3e-19;

Matches 78; Conservative 55; Mismatches 147; Indels 1; Gaps 1;

Qy 269 KIGFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVWSTCDITF 328

Db 3 RIGFVGITGMGPMAMNLLKAGHQVKVWVRTSSKAVSLKEAGAVCSLEQVQKDVFLI 62

Qy 329 ACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388

Db 63 CMLS DGKTCDBILFQERGAISQLPVESTVIYMSSIPVEVAKKQSEKCKENGLRYLDAPVS 122

Qy 389 GNOQLSNDGMLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLIVNMQGSFM 448

Db 123 GGEKAQNASLAIWVGDAQTFSHAEHVLAMGR-PILVGAAGCGMLAKLWNQIVASTI 181

Qy 449 ATIAEGLTLAHVTGOSQOITLLDILNQGLASIFLDQKQNTLOGNFKPFDYLVKVIQKDLR 508

Db 182 ATVSEGLLLASKAGADPIKLAQLTGGFADSPILQQHGERMLNRDFKPGGTARNCHKDII 241

Qy 509 LAIALGDVAVNHTPMAAAANEVYKRAKALDOSDNDMSAVYR 549

Db 242 TAVSYAKSLNLPLTIAQVSQLFENMLAAGDGLDHSGLIR 282

RESULT 30

US-10-282-122A-66301

; Sequence 66301, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 66301

; LENGTH: 288

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66301

Query Match 11.3%; Score 324.5; DB 12; Length 288;

Best Local Similarity 26.5%; Pred. No. 5.4e-19;

Matches 74; Conservative 62; Mismatches 142; Indels 1; Gaps 1;

Qy 270 IGFLGLGMLGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGA-RLGRTPAEVWSTCDITF 328

Db 4 VAFILGLTGMGPMAGHQLQREGYDVCVYNRSSAKALRWVEYAGRRADTPREACAGAEILVF 63

Qy 329 ACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388

Db 64 CCVGNDDDLRAVALGEQAGFAGMAPGSLFVDHTTTASAEVARELSLLAAERELGFLDAPVS 123

Qy 389 GNOQLSNDGMLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLIVNMQGSFM 448

Db 124 GGQAGAVNGALTVMVGGEEAFYRRAEPLLSYARMVRMGMVDVSGQLTKMVNQICVAGLL 183

Qy 449 ATIAEGLTLAHVTGOSQOITLLDILNQGLASIFLDQKQNTLOGNFKPFDYLVKVIQKDLR 508

Db 184 QGLAEALHFARCAGLDGEAMQVIGKGAASQWLENHQSLMAGEFPDFGFAVDMWRKDL 243

Qy 509 LAIALGDVAVNHTPMAAAANEVYKRAKALDOSDNDMSAV 547

Db 244 ILLAEARNGAQLPVTALVDQFYAEVQAMGGGRWDTSSL 282

Search completed: September 16, 2004, 07:44:09

Job time : 722 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2004, 07:28:53 ; Search time 19 Seconds

(without alignments)
2799.680 Million cell updates/sec

Title: US-10-067-482-2

Perfect score: 2866

Sequence: 1 MAAVSLRLGLVWGKLGKLYP.....AKALDQSDNMSAVYRIYIH 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 78:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	392.5	13.7	288	2	C70303 3-hydroxyisobutyra
2	392	13.7	289	2	G90314 oxidoreductase [lm
3	384	13.4	334	2	T08967 hypothetical prote
4	375	13.1	292	2	G97310 dehydrogenase rela
5	368	12.8	288	2	B69870 3-hydroxyisobutyra
6	367	12.8	299	1	JQ0613 3-hydroxyisobutyra
7	367	12.8	299	2	C91129 probable dehydroge
8	367	12.8	299	2	C85974 probable dehydroge
9	361	12.6	294	2	AE0897 2-hydroxy-3-oxopro
10	338	11.8	290	2	S76381 3-hydroxyisobutyra
11	335	11.7	291	2	AB3380 3-hydroxyisobutyra
12	334	11.7	296	2	T34859 probable dehydroge
13	333	11.6	286	2	AC1558 3-hydroxyisobutyra
14	331.5	11.6	299	2	B83979 3-hydroxyisobutyra
15	331	11.5	286	2	AE1200 3-hydroxyisobutyra
16	330	11.5	285	2	G71912 3-hydroxyisobutyra
17	329	11.5	289	2	B81065 probable 3-hydroxy
18	329	11.5	289	2	E81802 3-hydroxyacid dehy
19	324.5	11.3	288	2	F83447 hypothetical prote
20	318.5	11.1	315	2	H82512 probable 3-hydroxy
21	318	11.1	296	2	H83456 probable oxidoredu
22	318	11.1	315	2	A98338 D-threonine dehydro
23	318	11.1	315	2	AI2944 3-hydroxyisobutyra
24	316	11.0	293	2	G86901 3-hydroxyisobutyra
25	316	11.0	371	2	T10635 hypothetical prote
26	310	10.8	296	2	C83232 3-hydroxyisobutyra
27	309	10.8	294	2	B96015 probable 2-hydroxy
28	303.5	10.6	301	2	G96013 conserved hypothet
29	301.5	10.5	292	2	D64782 3-hydroxyisobutyra

30	301.5	10.5	297	2	E96736 probable dehydroge
31	299.5	10.5	292	2	B90700 carbinic semialde
32	299.5	10.5	292	2	B90700 probable oxidoredu
33	295	10.3	289	2	E85550 3-hydroxyisobutyra
34	295	10.3	299	2	D96736 probable dehydroge
35	293	10.2	291	2	D83371 probable dehydroge
36	293	10.2	293	2	G95277 Probable D-threoni
37	291.5	10.2	298	2	AI0947 probable oxidoredu
38	290	10.1	346	2	A32867 3-hydroxyisobutyra
39	288	10.0	286	2	E87444 conserved hypothet
40	287.5	10.0	298	2	S40826 hypothetical 31.2K
41	281.5	9.8	298	2	E91229 probable dehydroge
42	281.5	9.8	298	2	D86076 probable dehydroge
43	279.5	9.8	292	2	AB0567 2-hydroxy-3-oxopro
44	279.5	9.8	295	2	JC7926 3-hydroxyisobutyra
45	279	9.7	298	2	C96022 probable 3-hydroxy
46	278	9.7	313	2	AH3058 2-HYDROXY-3-OXOPRO
47	278	9.7	313	2	H98227 3-hydroxyisobutyra
48	270	9.4	300	2	AH2912 oxidoreductase [imp
49	270	9.4	300	2	C97687 D-threonine dehydr
50	269.5	9.4	302	2	AI3645 3-hydroxybutyrate
51	264.5	9.2	298	2	B83553 probable 3-hydroxy
52	263.5	9.2	310	2	AB3338 3-hydroxyisobutyra
53	261.5	9.1	298	1	C42902 3-hydroxyisobutyra
54	259.5	9.1	292	2	AG2225 3-hydroxyacid dehy
55	259.5	9.1	299	2	T18682 3-hydroxyisobutyra
56	254.5	8.9	295	2	A96019 probable dehydroge
57	253	8.8	304	2	AC3064 3-hydroxyisobutyra
58	253	8.8	304	2	H98222 probable [imported
59	252	8.8	295	2	H95295 probable 2-hydroxy
60	245.5	8.6	296	2	AI0443 protein F15H18.21
61	244.5	8.5	1197	2	D86317 hypothetical prote
62	239	8.3	302	2	D65054 3-hydroxyisobutyra
63	234.5	8.2	294	2	B70825 3-hydroxyisobutyra
64	224.5	7.8	261	2	A69807 3-hydroxyisobutyra
65	213.5	7.4	298	2	C87417 3-hydroxyisobutyra
66	209.5	7.3	295	2	E70707 hypothetical prote
67	203	7.1	287	2	E72666 probable 3-hydroxy
68	201.5	7.0	310	2	H75510 3-hydroxyisobutyra
69	198	6.9	301	2	B64164 hypothetical prote
70	189	6.6	203	2	JC7163 hepatoma-derived g
71	186.5	6.5	237	2	JC5660 hepatoma-derived g
72	185.5	6.5	240	2	A55055 hepatoma-derived g
73	168.5	5.9	1392	2	T51947 probable transcrip
74	162	5.7	472	2	AD1609 6-phosphogluconate
75	162	5.7	472	2	AH1246 6-phosphogluconate
76	160.5	5.6	669	2	JC5662 hepatoma-derived g
77	159.5	5.6	530	2	JC7168 lens epithelium-de
78	157.5	5.5	304	2	S59414 hypothetical prote
79	154.5	5.4	476	2	AC2465 6-phosphogluconate
80	149	5.2	1445	2	T50508 hypothetical prote
81	148.5	5.2	1360	2	JC5839 GTBP-N protein - h
82	146.5	5.1	632	2	T48316 hypothetical prote
83	146	5.1	468	2	AI1250 phosphogluconate d
84	141.5	4.9	484	2	T01658 phosphogluconate d
85	141	4.9	468	2	D56146 phosphogluconate d
86	140	4.9	468	2	162463 phosphogluconate d
87	139.5	4.9	511	2	T05363 phosphogluconate d
88	139	4.8	468	2	I84555 phosphogluconate d
89	139	4.8	468	2	I41249 phosphogluconate d
90	139	4.8	468	2	F90982 gluconate-6-phosph
91	139	4.8	468	2	D85828 gluconate-6-phosph
92	138.5	4.8	492	2	T25520 6-phosphogluconate
93	137	4.8	1095	2	T25520 hypothetical prote
94	136.5	4.8	482	1	D81659 phosphogluconate d
95	136	4.7	468	1	DESGC 6-phosphogluconate
96	135.5	4.7	483	2	D87167 probable phosphogl
97	135.5	4.7	486	2	T44750 microtubule-associ
98	135.5	4.7	2364	2	A56577 6-phosphogluconate
99	135	4.7	469	2	A72377 probable phosphogl
100	134.5	4.7	508	2	T42523

ALIGNMENTS

RESULT 1
C70303
3-hydroxyisobutyrate dehydrogenase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C:Accession: C70303
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70303
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-288 <AOF>
A:Cross-references: GB:AE000670; NID:g2982779; PIDN:AA06408.1; PID:g2982783; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: htd
A:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
P;3-265/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
Query Match 13.7%; Score 392.5; DB 2; Length 288;
Best Local Similarity 31.7%; Pred. No. 9e-19;
Matches 90; Conservative 61; Mismatches 132; Indels 1; Gaps 1;
QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
DB 2 KVGFIGLHGRATKRLIEQGVETIWNRTLSKAHEFAKTEVTSPPADLINKVDV 61
QY 328 FACVSDPKAAKDLVLGSPGVLQGIKPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPV 387
DB 62 FVIVFDSQAEVIFGEKGLVKGDIKGTVIDMTNHYLYAKAYEELKCLGAFYLDAPV 121
QY 388 SGNQOLSDNGMLVILAAAGDRLGYEDCCSCFOAMGKTSFFLGEVGNAAKMLIVNMVQGSF 447
DB 122 LGSVIPALKGELTIVVGGDKFENKFLPFKFRATYILGAGMGSKMLVNMVILGGI 181
QY 448 MATAEGLTLAHVTGQSQTLLDILNOGLASIFLDQKQNILOQNFNFPDFVLYKIQKDL 507
DB 182 MEVLAETALGEKAGIDKETIIVNLNDGAGKSYLDVKKLLEDFSTHESVNIYKDL 241
QY 508 RLATLGDVAVNHTPTMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
DB 242 HYAQLIKDLGLFSFTTAAVKETGLARKEGFGNLDPSAVYKLF 285
RESULT 2
G90314
oxidoreductase [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: G90314
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.A.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <KUR>
A:Cross-references: GB:AE006641; NID:g13814790; PIDN:AAK41774.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1560
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 13.7%; Score 392; DB 2; Length 289;
Best Local Similarity 29.3%; Pred. No. 9.8e-19;

Matches 83; Conservative 68; Mismatches 132; Indels 0; Gaps 0;
QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
DB 2 KVGFIGLHGRATKRLIEQGVETIWNRTLSKAHEFAKTEVTSPPADLINKVDV 61
QY 329 ACVSDPKAAKDLVLGSPGVLQGIKPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
DB 62 SMWTDAPVEVLEFVGVNGVSKNKRGLIFVDMSTNSPEFAKVTIKRLSEYGMFLDAPVT 121
QY 389 GNOOLSDNGMLVILAAAGDRLGYEDCCSCFOAMGKTSFFLGEVGNAAKMLIVNMVQGSFM 448
DB 122 GSKGAREGLTITMVGKEDVFKRVEPIFKAMGNIIHVGDVSGQALKLCNQVVALNM 181
QY 449 ATTAEGTLTAHVTVGQSQTLLDILNOGLASIFLDQKQNILOQNFNFPDFVLYKIQKDLR 508
DB 182 VSVVEGELLARSIGIDDDKLFVSLTGAANSFTVQYLYPKIMKGDLPFGPKAAHLKKDLK 241
QY 509 LALATLGDVAVNHTPTMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
DB 242 YAMEIANSKSLPLGLTSLALQLYNAMVSLGIGELGTQGLVKVY 284
RESULT 3
T08967
hypothetical protein F19B15.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2000
C:Accession: T08967
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16519
A:Accession: T08967
A:Molecule type: DNA
A:Residues: 1-334 <BEV>
A:Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150
A:Experimental source: cultivar Columbia; BAC clone F19B15
C:Genetics:
A:Gene: ATSP:F19B15.150
A:Map position: 4
A:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
F;40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
Query Match 13.4%; Score 384; DB 2; Length 334;
Best Local Similarity 32.2%; Pred. No. 4e-18;
Matches 96; Conservative 48; Mismatches 150; Indels 2; Gaps 2;
QY 254 ADSTAVNGSIPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARL 313
DB 24 ASSTISSDIITPSNTKIGWIGVMSGCHLIKAGYTVTVFNRTISKAQTLIDMGANV 83
QY 314 GRTPAEVSTCDITFACVSDPKAAKDLVLGP-SGVLOGIRPGKCYVDMSTVDADTVTELA 372
DB 84 ADSPNSVAEQSDVFTVIVGSDVHLLDPKSGALSGRLRGVVLVDMTSEPSLAELIA 143
QY 373 QVIVSRGRFLEAPVSGNQQLSNDGMVILAAAGDRLGYEDCCSCFOAMGKTSFFLGEVGN 432
DB 144 KAASFNCFSIDAPVSGGDLGAKNKLISFAGGDETTVKRLDPLFSLMGKNV-FMGTSK 202
QY 433 AAKMMLIVNMVQGSFMATAGLTLTAHVTVGQSQTLLDILNOGLASIFLDQKQNILOQ 492
DB 203 GQFALANQITIASTMLGLVEGLIYAHKAGLDVKKFLFLEAISTGAAGSKSIDLYGDRILKR 262
QY 493 NEFKPDFLYKIQKDLRLALALGDVAVNHTPTMAAAANEVYKRAKALDQSDNDMSAVYRA 550
DB 263 DFDPGFVNHVFKDLGICLINECQRMGLALPGLALAAQLYLSLKAHEGEGDLGTQALLA 320
RESULT 4
G97310
dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC B. subtilis ortholog
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

Query Match 12.8%; Score 368; DB 2; Length 288;
Best Local Similarity 26.7%; Pred. No. 3.0e-17;
Matches 76; Conservative 65; Mismatches 144; Indels 0; Gaps 0;

QY 268 KKIGFLGLGMSGIYSNLLKMGHTVTVMNRATAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
3 KIIGFVLGVGMGSMASHIILNDGHFVLIVYTRTEKAESILOKGAIWKDTVKDLSKADVI 62

QY 328 FACVSDPKAAKDLVLPGSGVLQGIRPGKCVCYVDMGTVDADTVELAQVIVSRGRFLEAPV 387
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
63 ITWMVGYPDSVEEYVFVNGSIENAEKAGAYLIDMTTSKPSLAKKTAEAKEKALFALDAPV 122

QY 388 SGNQQLSNDGMLVILAAGDRGLVEDCCSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
123 SGGDIGAONGTLAIMVGGEKEAFACMIPISLMGENIQYQGPAGSGQHTKMCNQIAAAG 182

QY 448 MATIAEGLTLAHVTGQSQQOTLLDILNOQLASIFLDQKCNLOLNFKPDPYLKVIQKDL 507
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
183 MLGVAEMAYAQSGLPEPNLVKSITTTGAAGSWLSNLAPRMLOGNFPFGFYVGHFXDKM 242

QY 508 RLAILGDVANNHPTPMAAANEEVYKRAKALDQSDNDMSAVVRAYI 552
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
243 GIALFEAEELMBEMPGLSLAKSLDYKLAAQGEENSQTQSIYKLWV 287

RESULT 6

JQ0613

N:hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli (strain K-12)
3:Alternate names: hypothetical 31k protein (rnpB-sohA intergenic region)
C:Species: Escherichia coli
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
J:Accession: JQ0613; A65102
R:Komine, Y.; Inokuchi, H.
Submitted to JIPID, September 1990
A:Reference number: JQ0612
A:Accession: JQ0613
A:Molecule type: DNA
A:Residues: 1-299 <KOM>
A:Experimental source: strain K12, W3110
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65102
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <BLAT>
A:Cross-references: GB:ABR000394; GB:U00096; NID:q2367197; PIDN:AAC76159.1; PID:g1789513;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yhaE
C:Map position: 68 min
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
C:Keywords: oxidoreductase
F:8-269/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match 12.8%; Score 367; DB 1; Length 299;
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;

QY 269 KIIGFLGLGMSGIYSNLLKMGHTVTVMNRATAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
7 KVGFILGIMGKPSKNLLKAGYSLVVADRNPPEATDVIAAGETASTAKATAEQCDVII 66

QY 329 ACVSDPKAADLVLPGSGVLQGIRPGKCVCYVDMGTVDADTVELAQVIVSRGRFLEAPVS 388
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
67 TMLPNSPHVKEVALGENGIIIEGAKPGTVLI DMSSIAPLASREISEALKAKGIDMLDAPVS 126

QY 389 GNQQLSNDGMLVILAAGDRGLVEDCCSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
Db |||:|||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:
127 GGEPKALDGTLSSVWGDDKAIFDKYDLYMKAMAGSVVHTGISIGNVT/KLANQVIALNI 186

C;Genetics:
A:Gene: yhaE
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
Query Match 12.8%; Score 367; DB 2; Length 299;
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 187 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 246
QY 509 LAIALGDVAVNHTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
Db 247 NALDTSHGVAQLPLTAAVMMQALRADGLGTADHSALACY 288
RESULT 7
C91129
probable dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C91129
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; PMID:21156231; PMID:11258796
A;Accession: C91129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA037426.1; PID:gl3363476; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A:Gene: ECs4003
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 12.8%; Score 367; DB 2; Length 299;
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;
QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db 7 KVGFIGLGMKPMKSNLLKAGSVLVADNPEAIADVIAAGAEASTAKAEQCDVII 66
QY 329 ACVSDPKAAKDLVLGPGSVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
Db 67 TMLPNSPHVKEVALGNGIIEGAKPGTGLVDMSSIAPLASREISEALKAKGIDMLDAPVS 126
QY 389 GNOQLSNDGMVLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIWNVQGSFM 448
Db 127 GGEPKAIDGTLVSVWVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 186
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 187 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 246
QY 509 LAIALGDVAVNHTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
Db 247 NALDTSHGVAQLPLTAAVMMQALRADGLGTADHSALACY 288
C;Genetics:
A:Gene: ECs4003
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 12.8%; Score 367; DB 2; Length 299;
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;
QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db 7 KVGFIGLGMKPMKSNLLKAGSVLVADNPEAIADVIAAGAEASTAKAEQCDVII 66
QY 329 ACVSDPKAAKDLVLGPGSVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
Db 67 TMLPNSPHVKEVALGNGIIEGAKPGTGLVDMSSIAPLASREISEALKAKGIDMLDAPVS 126
QY 389 GNOQLSNDGMVLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIWNVQGSFM 448
Db 127 GGEPKAIDGTLVSVWVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 186
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 187 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 246
QY 509 LAIALGDVAVNHTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
Db 247 NALDTSHGVAQLPLTAAVMMQALRADGLGTADHSALACY 288
C;Genetics:
A:Gene: ECs4003
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 12.8%; Score 367; DB 2; Length 299;
Best Local Similarity 29.4%; Pred. No. 1.1e-16;
Matches 80; Conservative 58; Mismatches 141; Indels 0; Gaps 0;
QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db 2 KVGFIGLGMKPMKSNLLKAGSVLVADNPEAIADVIAAGAEASTAKAEQCDII 61
QY 329 ACVSDPKAAKDLVLGPGSVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
Db 62 TMLPNSPHVKEVALGNGIIEGAKPGTGLVDMSSIAPLASREISEALKAKGIDMLDAPVS 121
QY 389 GNOQLSNDGMVLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIWNVQGSFM 448
Db 122 GGEPKAIDGTLVSVWVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 181
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 182 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 241

C;Genetics:
A:Gene: yhaE
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
Query Match 12.8%; Score 367; DB 2; Length 299;
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;
QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db 7 KVGFIGLGMKPMKSNLLKAGSVLVADNPEAIADVIAAGAEASTAKAEQCDVII 66
QY 329 ACVSDPKAAKDLVLGPGSVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
Db 67 TMLPNSPHVKEVALGNGIIEGAKPGTGLVDMSSIAPLASREISEALKAKGIDMLDAPVS 126
QY 389 GNOQLSNDGMVLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIWNVQGSFM 448
Db 127 GGEPKAIDGTLVSVWVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 186
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 187 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 246
QY 509 LAIALGDVAVNHTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
Db 247 NALDTSHGVAQLPLTAAVMMQALRADGLGTADHSALACY 288
RESULT 9
AE0897
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) [imported] - Salmonella enterica subsp
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0897
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:21534947; PMID:11677608
A;Accession: AE0897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07771.1; PID:gl6504320; GSPDB:GN00176
C;Genetics:
A:Gene: gar
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
C;Keywords: oxidoreductase
Query Match 12.6%; Score 361; DB 2; Length 294;
Best Local Similarity 28.7%; Pred. No. 1.1e-16;
Matches 80; Conservative 58; Mismatches 141; Indels 0; Gaps 0;
QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
Db 2 KVGFIGLGMKPMKSNLLKAGSVLVADNPEAIADVIAAGAEASTAKAEQCDII 61
QY 329 ACVSDPKAAKDLVLGPGSVLQIRPGKCYVDMSTVDADTVTELAQVIVSRGRFLEAPVS 388
Db 62 TMLPNSPHVKEVALGNGIIEGAKPGTGLVDMSSIAPLASREISEALKAKGIDMLDAPVS 121
QY 389 GNOQLSNDGMVLVILAAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIWNVQGSFM 448
Db 122 GGEPKAIDGTLVSVWVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 181
QY 449 ATTAEGLTLAHVTGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 508
Db 182 AMSEALTATKAGVNPDLVYQAIRGGLAGSTVLDKAPVMVMDRNFPGFRIDLHIKDLA 241

Qy 509 LAIALGDVAVNHPTMAAAANEVYKRAKALQSDNDMSAV 547
Db 242 NALDTSHGVAQLPLTAAVMMQMALRADGNGNDHSAI 280

RESULT 10
S76381

Probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) - *Synechocystis* sp. (strain PQ)
C/Species: *Synechocystis* sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C/Accession: S76381
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S76381
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-290 <KAN>
A/Cross-references: EMBL:D64000; GB:AB001339; NID:gl0011484; PIDN:BAA10233.1; PID:gl00160
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
C/Keywords: oxidoreductase
F/6-267/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match	11.8%;	Score 338;	DB 2;	Length 290;	
Best Local Similarity	29.6%;	Pred. No. 3.8e-15;			
Matches	85;	Conservative 50;	Mismatches 144;	Indels 8;	Gaps 3;
QY	269	KIGFLGILMGSGIVSNLLKMGHTVTVWNRATKCDLFTQEGARLG----	RTPAEVVSTC	324	
Db	5	KIAVFLGVNGSPMAQLNKVNGQTVGYNRTLRPS--VQEAAGAGVKVVTISIAVAANA	62		
QY	325	DIITFACVSPDKAAKDLVLGPGSVLQIGRPGKCVDMSTVDATVTETLAQVIIVSRGRFLE	384		
Db	63	DIILTCVGEKQVQQLGSGGIAEYAKPQALIIDCSITTKTAAYELATNLKQLGRFLD	122		
QY	385	APVSGNQQLSNDGMLVILAAGDRGLVEDCSSCFQAMGKTSFFLGEVGNAAKMWLVNVMVQ	444		
Db	123	APVTGDDVGAINGTLTIWVGGIISDFEELPVLKSIGEKIVHCGSPSGSQAVKLCNQVLIC	182		
QY	445	GSMFMTAIEGLTLAHVTGOSQOITLIDLNQGOGLASIFLDQKQNTILQGNFKPDFLVKTIQ	504		
Db	183	GTHATAAAEAIQLSLEQLGIAPELVIDTCGSGAAGSWALTNLAPKMSADFAECFVWKHL	242		
QY	505	KDLRLAIALGDVAINHPTPMAAANEVYKRAKALDOSDNDMSAVYRAY	551		
Db	243	KDLRLVREA--AENGLPGVTTLAESLFTSVOLLGGEDOGSOAIRAY	287		

RESULT 11
AB3380
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) [imported] - *Brucella melitensis* (strain
C:Species: *Brucella melitensis*
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AB3380
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesha
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52205.1; PID:gl7982987; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11024
A:Map position: I

C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase homologues
C;Keywords: oxidoreductase

[illegible]

```

RESULT 12
T34859
C:Probable dehydrogenase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
C:Accession: T34859
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1999
A:Reference number: Z21559
A:Accession: T34859
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-296 <OLI>
A:Cross-references: EMBL:AL035478; PIDN:CAB36613.1; GSPDB:GN00070; SCOEDB:SC205.26c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC205.26c
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase
F:7-268/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

```

[illegible]

```
RESULT 13
AC1558
3-hydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lin1004 [imported]
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1558
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1558
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:g16413463; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1004
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 11.6%; Score 333; DB 2; Length 286;
Best Local Similarity 26.4%; Pred. No. 7.9e-15;
Matches 75; Conservative 61; Mismatches 148; Indels 0; Gaps 0;
QY 268 KKIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
DB 2 EKIGFVGTVGMSSMAXHLEAGYEVHYTRTKAEALLSQGLWESDPGSLGAKVDIL 61
QY 328 FACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLAPV 387
DB 62 ISMVGYPKDVEQLXILGNGFLDNKAGSVAIDMTTSSPALAKKIAEAGHEKIGVLDAPV 121
QY 388 SGNQQLSNDGMVLVLAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMVLIVNVQGSF 447
DB 122 SGDIGAKNGTLLAHVWGAEVFLKVKFIFELGSSVILQDAGSGQHTKMNQIAIASN 181
QY 448 MATIAEGLTLAHVTGQSQOTLLDILNQQLASIFLDQKCNILQGNFKPDFVKYIQKDL 507
DB 182 MGVTEAIIYABRAGLNPSRVLDISGGAAGWSLTNLIPRVLDQDFSPGFIFKFIKDM 241
QY 508 RLAIALGDVNHPTPMAAANEVYKRAKALDOSDNDMSAVYRAY 551
DB 242 GIALSEAKQMGLELPLGLTLAEQMYQTALAEQGLSEBGTQALIKYY 285
RESULT 14
B83979
3-hydroxyisobutyrate dehydrogenase BH2634 [imported] - Bacillus halodurans (strain C-125
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83979
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83979
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA06353.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2634
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 11.6%; Score 331.5; DB 2; Length 299;
Best Local Similarity 29.8%; Pred. No. 1.1e-14;
Matches 84; Conservative 47; Mismatches 150; Indels 1; Gaps 1;
```

```
QY 268 KKIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
DB 3 QKGVFVGLTGMGLPMTKHLVDKGFETYVTKSRSGPIBEALIOYGAIEVESYKELMETADIV 62
QY 328 FACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLAPV 387
DB 63 MTCLELPETVIDVYEGEDGHIAGLSQOKILIDHSTVDRETNVRVAEQIKEGGAFDAPV 122
QY 388 SGNQQLSNDGMVLVLAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMVLIVNVQGSF 447
DB 123 SGGPMGAKAGTLLITMCGEADSPERSKEVLGAYGDIYHVGPIGSGTVKVLANNVIGVH 182
QY 448 MATIAEGLTLAHVTGQSQOTLLDILNQQLASIFLDQKCNILQGNFKPDFVKYIQKDL 507
DB 183 QAVLGECLYFVEKAGVDPATAYEIIKRSAGFSKSMESVDAILDRAFDPRFSINLLHKDI 242
QY 508 RLAIALGDVNHPTPMAAANEVYKRAKALDOSDNDMSAVV 549
DB 243 GLALKLGEQLGLEPMEVKEERVAAKE-QYGHEDVSAIIR 283
RESULT 15
AE1200
3-hydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lmo1005 [imported]
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AE1200
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <GLA>
A:Cross-references: GB:NC 003210; PIDN:CAC99083.1; PID:g16410407; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1005
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 11.5%; Score 331; DB 2; Length 286;
Best Local Similarity 27.1%; Pred. No. 1.1e-14;
Matches 77; Conservative 59; Mismatches 148; Indels 0; Gaps 0;
QY 268 KKIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
DB 2 EKIGFVGTVGMSSMAXHLEAGYEVHYTRTKAEALLDQGLWVETPGSLANKVDIL 61
QY 328 FACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLAPV 387
DB 62 ISMVGYPKDVEQLXILGNGFLDNKAGSVAIDMTTSSPALAKKIAEAGHEKIGVLDAPV 121
QY 388 SGNQQLSNDGMVLVLAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMVLIVNVQGSF 447
DB 122 SGDIGAKNGTLLAHVWGAEVFLKVKFIFELGSSVILQDAGSGQHTKMNQIAIASN 181
QY 448 MATIAEGLTLAHVTGQSQOTLLDILNQQLASIFLDQKCNILQGNFKPDFVKYIQKDL 507
DB 182 MGVTEAIIYABRAGLNPSRVLDISGGAAGWSLTNLIPRVLDQDFSPGFIFKFIKDM 241
QY 508 RLAIALGDVNHPTPMAAANEVYKRAKALDOSDNDMSAVYRAY 551
DB 242 GIALSEAKQMGLELPLGLTLAEQMYQTALAEQGLSEBGTQALIKYY 285
RESULT 16
G71912
probable 3-hydroxyacid dehydrogenase - Helicobacter pylori (strain J99)
```


C;Species: Helicobacter pylori
 A;Variety: Strain J99
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C;Accession: G71912
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A;Reference number: A71800; MUID:99120557; PMID:9923682
 A;Accession: G71912
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <ARN>
 A;Cross-references: GB:AE001491; GB:AE001439; NID:g4155127; PIDN:AAD06158.1; PID:g415512
 A;Experimental source: strain J99
 C;Genetics:
 A;Gene: jhp0585
 C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
 F;3-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
 Query Match 11.5%; Score 330; DB 2; Length 285;
 Best Local Similarity 32.7%; Pred. No. 1.2e-14;
 Matches 92; Conservative 46; Mismatches 137; Indels 6; Gaps 4;
 QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
 DB 2 KIGWIGLGQWGLPMVTRLLDGGIEVGVYNNRSPDKTAPISAKGVYNTAEIVRDYPIF 61
 QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTTVELAQVIVSRGRFLEAPVS 388
 DB 62 TMLUSD-KAALDAVLAPKFWQMSK-KIVVMNTIAPLESLSLEKTAQKHQATYLEAPVS 118
 QY 389 GNQOLSDNGMLVILAAGDRGLYEDCSSCFQAMGKTSFPLGEVGNAAKMLIVNMVQGSFM 448
 DB 119 GSVGAAGKAGALLIAGDEVEISKLPVLAHLSQTFYLGKVGQGTGAKLSINSLAQMG 178
 QY 449 ATTAEGTLTAHVTCGQQOQLDILNQGLASIFLDQKCONILQGNKFPDFYLYKVIQKDLR 508
 DB 179 VAYSEALLAKLGVDAESFLQIIGSGMNSPLFQAKKGMWLQDNYPAAPSLKLMAKDIR 238
 QY 509 LA-IALGDVANHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
 DB 239 LAKNEAGEAMK-LPFLFQAEELYSAEKLSGLGLDMAVY 277

RESULT 17
 B81065
 3-Hydroxyacid dehydrogenase NMB1584 [imported] - Neisseria meningitidis (strain MC58 ser
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Nov-2001
 C;Accession: B81065
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vanatnevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81065
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-289 <TET>
 A;Cross-references: GB:AE002059; GB:AE002098; NID:g7226832; PIDN:AAF41937.1; PID:g722683
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1584
 C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
 F;9-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
 Query Match 11.5%; Score 329; DB 2; Length 289;
 Best Local Similarity 30.0%; Pred. No. 1.5e-14;
 Matches 84; Conservative 52; Mismatches 140; Indels 4; Gaps 2;

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
 DB 8 QIGWIGLGQWGLPMVTRLLDGGIEVGVYNNRSPDKTAPISAKGVYNTAEIVRDYPIF 67
 QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTTVELAQVIVSRGRFLEAPVS 388
 DB 68 LMVSDYAAVCDIL---NGVRDGL-AGKIIVMNSTISPTENLAVKALVEAAGGQFAEAPVS 123
 QY 389 GNQOLSDNGMLVILAAGDRGLYEDCSSCFQAMGKTSFPLGEVGNAAKMLIVNMVQGSFM 448
 DB 124 GSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTTFHFGDVGKSGAKLVNLSLIGIFG 183
 QY 449 ATTAEGTLTAHVTCGQQOQLDILNQGLASIFLDQKCONILQGNKFPDFYLYKVIQKDLR 508
 DB 184 EAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKSLWANREFPPAFALKHASKDLN 243
 QY 509 LAIALGDVANHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
 DB 244 LAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVY 283
 RESULT 18
 E81802
 hypothetical protein NMA1773 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Nov-2001
 C;Accession: E81802
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
 ; Holroyd, S.; Jørgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Accession: E81802
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-289 <PAR>
 A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85001.1; PID:g7380415
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: NMA1773
 C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hon
 F;9-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
 Query Match 11.5%; Score 329; DB 2; Length 289;
 Best Local Similarity 30.0%; Pred. No. 1.5e-14;
 Matches 84; Conservative 52; Mismatches 140; Indels 4; Gaps 2;

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
 DB 8 QIGWIGLGQWGLPMVTRLLDGGIEVGVYNNRSPDKTAPISAKGVYNTAEIVRDYPIF 67
 QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPGKCYVDMSTVDADTTVELAQVIVSRGRFLEAPVS 388
 DB 68 LMVSDYAAVCDIL---NGVRDGL-AGKIIVMNSTISPTENLAVKALVEAAGGQFAEAPVS 123
 QY 389 GNQOLSDNGMLVILAAGDRGLYEDCSSCFQAMGKTSFPLGEVGNAAKMLIVNMVQGSFM 448
 DB 124 GSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTTFHFGDVGKSGAKLVNLSLIGIFG 183
 QY 449 ATTAEGTLTAHVTCGQQOQLDILNQGLASIFLDQKCONILQGNKFPDFYLYKVIQKDLR 508
 DB 184 EAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKSLWANREFPPAFALKHASKDLN 243
 QY 509 LAIALGDVANHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
 DB 244 LAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVY 283
 RESULT 19
 F83447
 probable 3-hydroxyisobutyrate dehydrogenase PA1576 [imported] - Pseudomonas aeruginosa (s
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: A98338

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <KUR>

A:CROSS-references: GB:AE007870; PIDN:AAK90227.1; PID:g15160240; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L_3303

A:Map position: linear chromosome

C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc

Query Match 11.1%; Score 318; DB 2; Length 315;
Best Local Similarity 27.0%; Pred. No. 9e-14;
Matches 75; Conservative 58; Mismatches 139; Indels 6; Gaps 2;

QY 268 KKIGFLGLMGSGIVSNLLKMCHTWTVMNRATKCDLFIQEGARLGRTPAEYVSTCIDIT 327
Db :
12 RDIAVIGTGIMGAPMAARLAAGFAVRANRRRAEKAAIILAEKGVRQAATTIDAAVEADV 71

QY 328 FACVSDPKAADLVLPSPGVLOGIRPGKCYDMSVDADTTVELAQVIVSRGGRFLEAPV 387
Db :
72 ICMSSGPVCDEVLLGFGSVSAMKPGSVLLVMSIPVDSAREQAQARAHRGVRIVDAVP 131

QY 388 SCNQQLSNDMLVILAAGDRGLVEDCSCTQAMGKTFFLGEVGNNAKMMLIVNMVGGSF 447
Db :
132 SGEGKAIEGTLMAGGEGQRVDALRPLNLCLGRVT-HVGPVCGSLAKLANQLIVAST 190

QY 448 MATIAEGLTLAHTVGQSQQOTLLDLINOGQLASIFLDQCKNILQGNFKPDFLYKIQKDL 507
Db :
191 ICVAEAUTLVEAGGDPAQVROALLGGFAESTVFRHGKRMEVGDFRPGGPAKYQVKDT 250

QY 508 RLAIALGDVNHPTPMAAANAENVYKR-----AKALDQS 540
Db :
251 STALAFAXSRGLSLPVGEEVDRLFRSMVEHAGELDHS 288

RESULT 23

AI2944

3-hydroxyisobutyrate dehydrogenase mmsB [imported] - Agrobacterium tumefaciens (strain C)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C:Accession: AI2944

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan; ; Karp, P.; Romero, P.; Zhang, S.

I Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AI2944

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <KUR>

A:CROSS-references: GB:AE008689; PIDN:AAL43975.1; PID:g17741531; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: mmsB

A:Map position: linear chromosome

C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc

Query Match 11.1%; Score 318; DB 2; Length 315;
Best Local Similarity 27.0%; Pred. No. 9e-14;
Matches 75; Conservative 58; Mismatches 139; Indels 6; Gaps 2;

QY 268 KKIGFLGLMGSGIVSNLLKMCHTWTVMNRATKCDLFIQEGARLGRTPAEYVSTCIDIT 327
Db :
12 RDIAVIGTGIMGAPMAARLAAGFAVRANRRRAEKAAIILAEKGVRQAATTIDAAVEADV 71

QY 328 FACVSDPKAADLVLPSPGVLOGIRPGKCYDMSVDADTTVELAQVIVSRGGRFLEAPV 387
Db :
72 ICMSSGPVCDEVLLGFGSVSAMKPGSVLLVMSIPVDSAREQAQARAHRGVRIVDAVP 131

Qy 449 ATIAEGLTLAHTVGSGQQTLLDI-INQGOLASIFLDKQCQNUL-----QGNEKP-DFYLK 501
Db 182 IVACNALVIAEVAALAEAGVDASIVAPALAGGAFADSKPLQLIILAPQMAESRYZPVKHVR 241
Qy 502 YIQDRLRAIALGDVAVNHPTMAAAANVEYKRAKALDQSDNDMSAVYRAY 551
Db 242 TLLKOLDLTAVKLRSQGAATPMSGAAQLMRLHGSQGYLERDPATLVEQY 291

RESULT 27
B96015
Probable 2-hydroxy-3-oxopropionate reductase [SC 1.1.1.60] [imported] - Sinorhizobium me
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C:Accession: B96015
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A>Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B96015
A>Status: preliminary
A:Molecule_type: DNA
A:Residues: 1-294 <KUR>
A:Cross-references: GB:AL591985; PID:CAC49786.1; PID:gl5141273; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
lla, Hymen, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.G.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
neault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.,
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039 MUID:21368234; PMID:11474104

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A:Gene: glxR; SMD20679
A:Genome: plasmid
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h
C:Keywords: oxidoreductase

Query Match          10.8%; Score 309; DB 2; Length 294;
Best Local Similarity 26.3%; Pred. No. 3.2e-13;
Matches 74; Conservative 53; Mismatches 154; Indels 0; Gaps 0;

270 IGFLGILGMSGGIVSNLLKGHTTVMNRITAEKCDLFIQEGARLGRTPAEVSTCDITFA 329
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
280 IGFIIGIMGTPMARHQLQDAGHEIITSKFVIPPQRELVENGLEIVETPKALAEVTDITIL 63
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
330 CVSDPKAAKDLVLGPGSVLQGIREFGKCYVDMSTVDADTWTTELAQVIVSRGGREFLEAPVSG 389
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
390 NQOLSNDGMVILAAGRGLYEDGSSCPQAMGKTSFFLGEVGNAAKMMLIVNVQGSFWA 449
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
424 GEVAKNASLSINAGGKPSSEPALPLFLKMGKNITLVGDCGDGQVTVKANOIIVALTIE 183
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
450 TIAEGLTLAHTVGOSQOTLLDILNQGLASFLDQKCNILQGNFKPDPFLVKYIKDLRL 509
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
484 AVSSALYFASKAGADPARVREALMGGFASSRILEVHGDRMIKRTFEPGFRISLHQDLNL 243
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
510 AIALGDVNVHPTMAAANAENVYKRAKALDQSDNDMSAVVRA 550
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
524 ALQAKSLGISLPTATQELFNNCANGDGLDHSGLVRA 284
||||:||||: : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 28
G96013
conserved hypothetical protein Smb20668 [imported] - Sinorhizobium meliloti (strain 102
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: G96013
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna

```

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G96013
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49775.1; PID:G151141262; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20668
A:Genome: plasmid
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
Query Match 10.6%; Score 303.5; DB 2; Length 301;
Best Local Similarity 26.4%; Pred. No. 7.7e-13;
Matches 75; Conservative 56; Mismatches 152; Indels 1; Gaps 1;
QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFTQEGARLGRTPAEVWSTCDITF 328
DB 4 KIAVLGLSGMGFGACSMKSLAGLDVLGYDVAPPAVERFVAGRGAGTPGAVTGADIIV 63
QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGRFLFAPVS 388
DB 64 SIVVSGAQTEAVLFGPNVAGAKPGAAFISSATMDPAIRDLAQRLEALGHYLDAPIS 123
QY 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFPL-GEVGNAAKMMLIVNVQGSF 447
DB 124 GGAAGAAGELTIVASGSPQFAAPALDAAKAVVELGCTAGTGAAAFKMINQLLAGVH 183
QY 448 MATTAEGTLAHTVGTGSOQTLLDILNQGLASIFLDQKCONILQGNFKPDFYLYKIQKDL 507
DB 184 IAAACEAIAFAKQGLDLKVEVITASAGNSWFWFENRIPHLVAGDVAPLSAIEIFVKDL 243
QY 508 RLALAGDVAHVHPTMAAANEVYKRAKALDQSDNMSAVYRAY 551
DB 244 GIVQDMARAEYPPVPLVAAALQMTYLAASGAGMGRRDDSSLARLY 287
RESULT 29
D64782
3-hydroxyisobutyrate dehydrogenase homolog b0509 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: D64782
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D64782
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-292 <BLAT>
A:Cross-references: GB:AE000157; GB:U00096; NID:G1786716; PIDN:AAC73611.1; PID:G1786719;
A:Experimental source: strain K-12, substrain MGL655
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
F;3-263/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
Query Match 10.5%; Score 301.5; DB 2; Length 292;
Best Local Similarity 27.7%; Pred. No. 1e-12;
Matches 78; Conservative 51; Mismatches 152; Indels 1; Gaps 1;
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DB 2 KLGFLGIGMGTPMAINLARAGHQLHV-TTIGPVADELLSLGAVSVETARQVTHEADIIF 60
QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGRFLFAPVS 388
DB 61 INVPTDTPQVEEVLFGENGCTKASLAKGKTIVDMSSISPIETKRFARQVNLGGDYLDPV 120
QY 389 GNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFPLGEVGNAAKMMLIVNVQGSF 448
DB 121 GGEIGARETSLIMVGGDEAVFERVKPFLGLGKNITLVGGNGDQGTCKVANQIIVALNI 180
QY 449 ATIAEGLTLAHTVGTGSOQTLLDILNQGLASIFLDQKCONILQGNFKPDFYLYKIQKDL 508
DB 181 EAVSEALLFASKAGADPVVRQALMGWGFASSRILEVHGEMIKRTFNFQFKIALHOKDLN 240
QY 509 LAIALGDVAHVHPTMAAANEVYKRAKALDQSDNMSAVYRA 550
DB 241 LALQSAKALALNLTATCOELFNTCAANGGSQLDHSALVQA 282
RESULT 30
E96736
Probable dehydrogenase F23N20.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E96736
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <STO>
A:Cross-references: GB:AE005173; NID:G6714326; PIDN:AAF26019.1; GSPDB:GN00141
C:Genetics:
A:Gene: F23N20.17
A:Map position: 1
C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hon
Query Match 10.5%; Score 301.5; DB 2; Length 297;
Best Local Similarity 28.3%; Pred. No. 1e-12;
Matches 76; Conservative 56; Mismatches 130; Indels 7; Gaps 2;
QY 263 ITPDXXKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFTQEGARLGRTPAEVVS 322
DB 9 IDPSKTRIGIGIGIMSAMVSHIIAAGYSVTVVARDLRKTLQTKGARIANSFKELAE 68
QY 323 TCDITFACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTELAQVIVSRGRF 382
DB 69 MSDVFTVTVGNFNDVRSLLGDDGVLSGLTPGGTVDMTSSKPLAREIHAEARRNCWA 128
QY 383 LEAPVSGNOQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFPLGEVGNAAKMMLIVNV 442
DB 129 VDAVSGDAGAREGTIGIFAGGDSSEIVELWSPVKNIG-TVTVMGAGGSGQSKGNQI 187
QY 443 VQGSFWATIAEGLTLAHTVGTGSOQTLLDILNQGLASIFLDQKCONILQGNFKPDFYLYK 502
DB 188 AGASNLVGLAEGIVFAEKAGLDTVKMLEAVKDGAGSVMVRLFGEMIVKEDYRATGA 247
QY 503 IQKDLRLALATAGDVAHVHPTMAAANEVY 531
DB 248 MVKD-----LGMVAABAMPGAALSKQLF 270
Search completed: September 16, 2004, 07:31:11

us-10-067-482-2.rpr

Thu Sep 16 09:36:52 2004

Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:28:53 ; Search time 13 Seconds
(without alignments)
2214.984 Million cell updates/sec

Title: US-10-067-482-2

Perfect score: 2866

Sequence: 1 MAAYSLRLGLVWKGKLRYP.....AKALDQSDNDSAVRAYIH 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	12.8	288	1	YKWC_BACSU
2	367	12.8	294	1	GARR_ECOLI
3	338	11.8	290	1	Y229_SYNY3
4	328	11.4	347	1	D3HI_ARATH
5	301.5	10.5	292	1	Q9SUC0 arabidopsyt
6	297	10.4	335	1	P77161 escherichia
7	290	10.1	335	1	Q99113 mus musculus
8	289.5	10.1	298	1	D3HI_RAT
9	287.5	10.0	298	1	YIHU_SALTY
10	281	9.8	336	1	YIHU_ECOLI
11	278.5	9.7	324	1	D3HI_HUMAN
12	261.5	9.1	298	1	D3HI_DROME
13	259.5	9.1	299	1	MMSB_PSEAE
14	239	8.3	302	1	DH31_CABEL
15	234.5	8.2	284	1	YGBJ_ECOLI
16	224.5	7.8	261	1	MMSB_MYCTU
17	209.5	7.3	295	1	YFJR_BACSU
18	198	6.9	301	1	YGBJ_HAEIN
19	186.5	6.5	237	1	HDGF_MOUSE
20	185.5	6.5	237	1	HDGF_MOUSE
21	185.5	6.5	240	1	YCY3_SHEFR
22	148.5	5.2	1360	1	MSH6_HUMAN
23	146	5.1	468	1	6PGD_ECOLI
24	145.5	5.1	1358	1	MSH6_MOUSE
25	143.5	5.0	485	1	6PGD_CUNEL
26	141	4.9	468	1	6PGD_CUNEL
27	138.5	4.8	492	1	6PGD_SCHPO
28	137	4.8	468	1	6PGD_SHIFL
29	136	4.7	468	1	6PGD_ECOLI
30	135.5	4.7	1427	1	MES4_DROME
31	135.5	4.7	2459	1	MAPE_RAT
32	132.5	4.6	470	1	6PGD_SYNP7
33	132.5	4.6	484	1	6PGD_HAEIN

34	132	4.6	468	1	6PGD_SALTY
35	129.5	4.5	468	1	6PGD_BACSU
36	129	4.5	445	1	6PGD_KLETE
37	129	4.5	598	1	CYL1_HUMAN
38	128.5	4.5	468	1	6PGD_BUCBP
39	127.5	4.4	517	1	6PGD_CANAL
40	127.5	4.4	1359	1	ATRX_CABEL
41	127	4.4	445	1	6PGD_CITAM
42	127	4.4	2567	1	M18B_HUMAN
43	125.5	4.4	479	1	6PGD_TRYBB
44	123.5	4.3	468	1	6PG2_BACSU
45	123	4.3	445	1	6PGD_CITR
46	123	4.3	467	1	6PGD_BACLI
47	123	4.3	468	1	6PGD_STAN
48	122.5	4.3	908	1	DM3A_MOUSE
49	122	4.3	368	1	6PGD_STAM
50	121.5	4.2	2144	1	GLT1_YEAS
51	120.5	4.2	488	1	6PGD_TREPA
52	120.5	4.2	909	1	DM3A_HUMAN
53	120	4.2	1186	1	PKCB_HUMAN
54	119.5	4.2	741	1	ERF2_PICPI
55	118.5	4.1	2464	1	MAPB_MOUSE
56	118	4.1	445	1	6PGD_ESCVU
57	118	4.1	468	1	6PGD_STAP
58	118	4.1	634	1	KNOB_PLAFG
59	117	4.1	445	1	6PGD_KLEPL
60	117	4.1	2696	1	NSD1_HUMAN
61	115	4.0	977	1	RBMF_HUMAN
62	115	4.0	1402	1	Y232_HUMAN
63	114.5	4.0	472	1	6PGD_LACLA
64	114.5	4.0	959	1	IF2_BRUME
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66	114	4.0	445	1	6PGD_CITDI
67	114	4.0	445	1	6PGD_SHIBO
68	114	4.0	445	1	6PGD_SHIDY
69	114	4.0	445	1	6PGD_SHISO
70	113.5	4.0	492	1	6PG2_YEAS
71	113	3.9	829	1	IF2_HAEIN
72	113	3.9	2332	1	PCLO_FMDVA
73	112.5	3.9	5085	1	PCLO_RAT
74	112	3.9	484	1	6PGD_ACTAC
75	112	3.9	494	1	SFR4_HUMAN
76	111	3.9	562	1	BS69_HUMAN
77	111	3.9	743	1	FTSK_CLOTE
78	111	3.9	1210	1	AF4_HUMAN
79	111	3.9	1362	1	BRD4_HUMAN
80	110.5	3.9	506	1	CDYM_HUMAN
81	110.5	3.9	543	1	TLPI_MOUSE
82	110.5	3.9	633	1	MLH_TEETH
83	110.5	3.9	1581	1	PPRE_HUMAN
84	110	3.8	875	1	ARS2_MOUSE
85	109.5	3.8	472	1	6PGD_LALCL
86	109.5	3.8	494	1	SFR3_MOUSE
87	109.5	3.8	1007	1	PR4B_HUMAN
88	109	3.8	700	1	TRDN_CANFA
89	109	3.8	907	1	IF2_VIBVU
90	109	3.8	907	1	IF2_VIBVY
91	109	3.8	1101	1	PHF2_HUMAN
92	109	3.8	1462	1	NKCR_HUMAN
93	109	3.8	2492	1	ATRX_PANTR
94	108.5	3.8	690	1	RHO_MICLU
95	108	3.8	481	1	6PGD_CERCA
96	108	3.8	611	1	SAH3_HUMAN
97	107.5	3.8	494	1	SFR3_RAT
98	107.5	3.8	705	1	TRDN_RABIT
99	107.5	3.8	780	1	CDL2_HUMAN
100	107.5	3.8	892	1	IF2_YERPE

ALIGNMENTS

RESULT 1

YKWC BACSU
ID YKWC BACSU STANDARD; PRT; 288 AA.
AC Q34948;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase YKWC (EC 1.1.-.-).
GN YKWC OR BSU13960.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Scanlan E., Devine K.M.;
RT "Sequence of the Bacillus subtilis chromosome from ykua to cse-15.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo F., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillette S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinot S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ222587; CAA10859.1; -
CC EMBL; Z99111; CAB13269.1; -
CC EMBL; B69870; B69870.
CC Subtilist; BG13328; YKWC.
CC InterPro; IPR002204; 3_hydroxyisobut_dh.
CC InterPro; IPR006183; 6PGD.
CC InterPro; IPR006115; 6PGD_NAD.
CC Pfam; PF03446; NAD_binding_2; 1.
CC PRINTS; PR00076; 6PGDHRGNASE.
CC PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT ACT SITE 172 BY SIMILARITY.
SQ SEQUENCE 288 AA; 30711 MW; 976DD098DBA7A30 CRC64;
Query Match 12.8%; Score 368; DB 1; Length 288;
Best Local Similarity 26.7%; Pred. No. 3.2e-16;
Matches 76; Conservative 65; Mismatches 144; Indels 0; Gaps 0;
QY 268 KKIGFLGLGLMGIVSNLLKMGHTVTVNNTAKKCDLFIQEGARLQGRTPAEVSTCDIT 327
DB 3 KTIQFGLGVGKMSVASHILNDGHPVLVYTKKAEKILQKGAIKWTKVDLSKADVI 62
QY 328 FACVSDPKAAKDLVLGPGSVLQGIIRPGKCYVDNSTVDADTVELAQVIVSGRFLRPAV 387
DB 63 ITWGYPSDVEEVFGSGIITENAKGAYLIDMTTSKPSLAKKIAEAAKALFALDAPV 122
QY 388 SGNQOLSNDGMLVILAGDRGLYEDSCFOAMGKTSFFLGEVGNAAKMLVNNVQGSF 447
DB 123 SGGDIGAQNGTLATWVGGEKAEACMPFISLMGENIQYQGPAGSGQHTKMCNQIAIAG 182
QY 448 MATTAEGGLTLAHVTGQSQQTLLDILNQGLASIFLDQKQNLQCNFKPDPFVLYKIQKDL 507
DB 193 MIGVAEMAYAKSGLEPENVLKSTTTGAAGSWSLSNLAPRMLQGNFEPGFVVKHFKDM 242
QY 508 RLATLGDVAVNHPPTMAAANEVYKRAKALDQSDNDMSAVYRAYI 552
DB 243 GIALEEAELMGEMPEGLSLAKSLYDKLAAQGEENSGTQSIYKLWV 287
RESULT 2
ID GARR_ECOLI STANDARD; PRT; 294 AA.
AC P23523;
DT 01-NOV-1991 (Rel. 20, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate
DE semialdehyde reductase) (TSAR).
GN GARR OR B3125 OR C3880.
OS Escherichia coli and
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=K12;
RC MEDLINE=91154140; PubMed=1705543;
RA Komine Y., Inokuchi H.;
RT "Precise mapping of the rnpB gene encoding the RNA component of RNase
RT P in Escherichia coli K-12.";
RL J. Bacteriol. 173:1813-1816(1991).
RN [2] SEQUENCE FROM N.A.
RP STRAIN=K12 / CFT073 / ATCC 700928;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3] SEQUENCE FROM N.A.
RP STRAIN=O6:HL / CFT073 / ATCC 700928;
RC MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).


```

RN [4]
RP CHARACTERIZATION.
RX MEDLINE=9847507; PubMed=9772162;
RA Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
RT "Evolution of enzymatic activities in the enolase superfamily:
RT characterization of the (D)-glucarate/galactarate catabolic pathway
RT in Escherichia coli.";
RL Biochemistry 37:14369-14375(1998).
RN [5]
RP GENE NAME.
RX MEDLINE=20225875; PubMed=10762278;
RA Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J.;
RT "A common regulator for the operons encoding the enzymes involved in
RT D-galactarate, D-glucarate, and D-glycerate utilization in
RT Escherichia coli.";
RL J. Bacteriol. 182:2672-2674(2000).
CC -1- CATALYTIC ACTIVITY: (R)-glycerate + NAD(P)(+) = 2-hydroxy-3-
CC oxopropanoate + NAD(P)H.
CC -1- PATHWAY: D-galactarate metabolism; third step.
CC -1- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D90212; BAA14238.1; ALT INIT.
DR EMBL; U18997; AAA57928.1; ALT INIT.
DR EMBL; AE000394; AAC76159.1; ALT INIT.
DR EMBL; AE016767; AAN82321.1; ALT_INIT.
DR EcoGene; EG11176; garR.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PFO3446; NAD binding 2; 1.
DR PRINTS; PR00076; 6EGDHRGNASE.
DR TIGRfams; TIGR01505; tartro_sem_red; 1.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
DR Oxidoreductase; NAD; Complete proteome.
KW ACT_SITE 170 170 BY SIMILARITY.
SQ SEQUENCE 294 AA; 30427 MW; 17DA392C2253278C CRC64;

Query Match 12.8%; Score 367; DB 1; Length 294;
Best Local Similarity 29.4%; Pred. No. 3.8e-16;
Matches 83; Conservative 57; Mismatches 140; Indels 2; Gaps 1;

QY 269 KIGFLGLGLMGSGIVSNLLKMGHTVTWNRTAEKCDLFIQEGARLGTPTAEVVSTCDITF 328
DB 2 KVGFIGLGGKPKSKNLLKAGSLVVDNRNPAIADVIAGAEETASTAKIAEQCDVII 61
QY 329 ACVSDPKAAKDLVLPGSGVLQGIKPKCYVDMSTVDADTVELAQVIVSGRGRFLAPVS 388
DB 62 TMLPNSPHVKEVALGNGIIEGAKPGTVLIDMSSIAPLASREISEALKAGIDMLDAPVS 121
QY 389 GNQQLSNDGMLVILAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAKMLIVNMVQSGFM 448
DB 122 GGEFPAIDGTLSVMVGDKAIFDKYDLMKAMAGSVVHTGEIGAGNVTKLANQVIVALNI 181
QY 449 ATIAEGLTLIAHVTGOSQQTLLDLILNQGLASIFLDQKCNILQGNFKPFPYLYKIDLR 508
DB 182 AMSEALTATKAGVNDPLVQYAIRGLAGSLVLDKAKPMVDRNPKPGFRIDLHIKDLA 241
QY 509 LATALGDVNHPTPMAAANEVYK--RAKALDQSDNDMSAVY 548
DB 242 NALDTSHGVAQLPLTAAVNMVMMQALRADGLGTADHSALACY 283

RESULT 3

```

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Y229 SYNY3
ID Q55702; STANDARD; PRT; 290 AA.
AC Q55702;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase slr0229 (EC 1.1.1.-.-).
GN SLR0229.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiura M., Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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CC
CC EMBL; D64000; BAA10233.1; -.
DR EMBL; S76381; S76381.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR Pfam; PFO3446; NAD binding 2; 1.
DR PRINTS; PR00076; 6EGDHRGNASE.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
DR Oxidoreductase; NAD; Complete proteome.
KW ACT_SITE 175 175 BY SIMILARITY.
SQ SEQUENCE 290 AA; 29930 MW; BB167CD4FCF4A37A CRC64;

Query Match 11.8%; Score 338; DB 1; Length 290;
Best Local Similarity 29.6%; Pred. No. 2.5e-14;
Matches 85; Conservative 50; Mismatches 144; Indels 8; Gaps 3;

QY 269 KIGFLGLGLMGSGIVSNLLKMGHTVTWNRTAEKCDLFIQEGARLG---RTPAEVVSTC 324
DB 5 KIAVFGLVGWSGPMQNLVKNVGYQTVGNRTLRPS--VQEAAGAGVYVTSIAVAANA 62
QY 325 DITFACVSDPKAAKDLVLPGSGVLQGIKPKCYVDMSTVDADTVELAQVIVSGRGRFLE 384
DB 63 DITLTGCGDEKDVQQLILSGSGGIAEYAKPQALIDCGTICKTAAYELATNLKQLGLRFLD 122
QY 385 APVSGNQQLSNDGMLVILAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAKMLIVNMVQ 444
DB 123 APTGSDVGAINGTLTIWVGDISDFEALPVUKSIGEKIVHCGPSGSGQAVKLCNQVLC 182
QY 445 GSEPMATIAEGLTLIAHVTGOSQQTLLDLILNQGLASIFLDQKCNILQGNFKPFPYLYKIQ 504
DB 183 GIHAIAAAEAQIQSEQLGIAPELVITCGSGAAGSWALTNLAPKMGSEADPAPGMVKHLL 242
QY 505 KDLRLAIALGDVNHPTPMAAANEVYKRAKALDQSDNDMSAVY 551
DB 243 KDLRLVREA--AENGPLPGVTTLAESLFTSVQLIGGEDQGSQAIRAY 287

RESULT 4
D3HI_ARATH
ID D3HI_ARATH STANDARD; PRT; 347 AA.
AC Q9SUC0; Q8LC25;
DT 16-OCT-2001 (Rel. 40, Created)

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RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 [2]
 RL SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
 RA Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
 RA Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBS databases.
 [3]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=K12 / ECL1;
 RA MEDLINE=20069628; PubMed=10601204;
 RX Cusa E., Obradors N., Baldoma L., Badia J., Aguilar J.;
 RT "Genetic analysis of a chromosomal region containing genes required
 RT for assimilation of allantoin nitrogen and linked glyoxylate
 RT metabolism in *Escherichia coli*";
 RL J. Bacteriol. 181:7479-7484(1999).
 CC -!- CATALYTIC ACTIVITY: (R)-glycerate + NAD(P) (+) = 2-hydroxy-3-
 CC oxopropanoate + NAD(P)H.
 CC -!- PATHWAY: Glyoxylate catabolism.
 CC -!- INDUCTION: By glyoxylate.
 CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
 CC family.
 CC
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 CC
 CC EMBL; AE000157; AAC73611.1; -
 CC DR EMBL; U82664; AAB40262.1; -
 CC DR EMBL; U89279; AAB93851.1; -
 CC DR PIR; D64782; D64782.
 CC DR EcoGene; EG13265; glxR.
 CC DR InterPro; IPR002204; 3hydroxisobut_dh.
 CC DR InterPro; IPR006183; 6PGD.
 CC DR InterPro; IPR006115; 6PGD_NAD.
 CC DR InterPro; IPR006398; Tartro_sem_red.
 CC DR Pfam; PF03446; NAD_binding_2; 1.
 CC DR PRINTS; PR00076; 6PGDHDRGNASE.
 CC DR TIGRFAMS; TIGR01505; tartro sem red; 1.
 CC DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
 KW Oxidoreductase; NAD; Complete proteome.
 FT ACT_SITE 169 169 BY SIMILARITY.
 SQ SEQUENCE 292 AA; 30800 MW; 5D5263231F2910F0 CRC64;
 Query Match 10.5%; Score 301.5; DB 1; Length 292;
 Best Local Similarity 27.7%; Pred. No. 4.8e-12;
 Matches 78; Conservative 51; Mismatches 152; Indels 1; Gaps 1;
 QY 269 KIGFLGILMGSGIVSNLLKMGHTVTVMNRATKCDLFIQEGARLGTAEVVTCDITF 328
 Db 2 KLGFGLIGMGTPMAINLARAGHQLHV-TTIGFVADELLSGAVSVETARQVTEASDIIF 60
 QY 329 ACVSDPKAKDLVLGPGSVLQGTIPGKCYDVMSTVDADVTVELAQIVTSGGRFLPAPVS 388
 Db 61 IMPVPTDPQVEEVFLFGNGCTKSLKKGITVDMSSISPIETKRFARQWELGGDYLDAPVS 120
 QY 389 GNOQLSNDGMLVTLAAGDRGLYEDCSCFOAMGKTSFFLGEVGNAAKMWLLVNMVQGSFM 448
 Db 121 GGIIGREGTSLWVGDEAVFERVPLFELLGNITLVGGNDGGDTCKVANOQIIVALNI 180
 QY 449 ATIAEGLTLAHVTGQSQTLLDILNQSLASIFLDQKQCNILQGNFKPDPFLYKVIQKDLR 508
 Db 181 EAVSEALLFASKAGADPVRVQALMGGFASSRILEVHGERMIKRTNFGFKIALHQKDLN 240
 QY 509 LATALGDVNHPTPMAAANEVYKRAKALDQSNQDMSAVTRA 550
 [1]
 [2]

Db 241 LALQSAKALALNLPNTATCQELFNTCAANGSQDLSALVQA 282
 RESULT 6
 DH31 MOUSE
 ID DH31 MOUSE STANDARD; PRT; 335 AA.
 AC Q99L13; Q9BJY2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
 DE (EC 1.1.1.31) (HIBADH).
 GN HIBADH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory organ;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragni T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Iwasanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

CC CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
CC CC methyl-3-oxopropanoate + NADH.
CC CC -!- SUBUNIT: Homodimer (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC CC family.
CC CC
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CC CC
CC CC EMBL; BC003914; AAH03914.1; -.
CC CC EMBL; AK078175; BAC37162.1; -.
CC CC PIR; PT0534; PT0534.
CC CC MGI; 1889802; 6430402H1ORik.
CC CC InterPro; IPR002204; 3hydroxisobut_dh.
CC CC InterPro; IPR006183; 6PGD.
CC CC InterPro; IPR006115; 6PGD_NAD.
CC CC Pfam; PF03446; NAD binding 2; 1.
CC CC PRINTS; PR00076; 6PGDHRGNASE.
CC CC PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
CC CC Oxidoreductase; NAD; Mitochondrion. Transit peptide.
CC CC TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).
CC CC CHAIN 36 335 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
CC CC NP_BIND 39 67 NAD (ADP PART) (POTENTIAL).
CC CC ACT_SITE 208 208 BY SIMILARITY.
CC CC CONFLICT 2 2 A -> S (IN REF. 1).
CC CC SEQUENCE 335 AA; 35440 MW; 5E9ECB03997DB110 CRC64;
CC CC
CC CC Query Match 10.4%; Score 297; DB 1; Length 335;
CC CC Best Local Similarity 26.1%; Pred. No. 1.1e-11;
CC CC Matches 81; Conservative 58; Mismatches 157; Indels 14; Gaps 4;
CC CC
CC CC QY 247 GSTSIQAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVMNRRTAEKCDLF 306
CC CC Db 25 GSLLAAVCSRSMA---SKTP---VGFGLGNMGNPMKLNKKGYPILLYDFPVDCKEF 77
CC CC
CC CC QY 307 IOEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGSPGVQLGIRPKCYVDMSTVDAD 366
CC CC Db 78 KEAGEQVASSPADVAEKADRIITMLPSSNNAVEVYSGANGILKKVKGSLIDSITDPS 137
CC CC
CC CC QY 367 TVTELAQVTVSRGGRFLEAPVSGNQLSNDGMVILAAAGDRGLYEDCSCFOAMGKTSFF 426
CC CC Db 138 VSKELAKEVEKMGAVFMDAPVSGVGAARSGNLTFMVGGVEDEFAAAQELLECMSGNVVY 197
CC CC
CC CC QY 427 LGEVGNAAKMLIVNVQGSFNTAIEGLTLAHTVCSQOTLLDILN--QGOLASIFLDQ 484
CC CC Db 198 CGAVGTGQSAKICNNMLLAISMTGTAEMNLGIRSLGDLPLAKILNMSGRCWSSDTYN 257
CC CC
CC CC QY 485 KCQNILQG-----NFKPFDLYKIQDLRLAIALGDVANHPTPMAAANEVYKAKALQD 539
CC CC Db 258 PFGVMHGVPSNNYQGGFTLMAKDLGLAQDSATSTKTPILLGLSLAHQIVRMCKSGY 317
CC CC
CC CC QY 540 SNDMSAVYR 549
CC CC Db 318 SKKDFSSVFQ 327
CC CC
CC CC RESULT 7
CC CC D3HI_RAT
CC CC ID D3HI_RAT STANDARD; PRT; 335 AA.
CC CC AC P29266;
CC CC DT 01-DEC-1992 (Rel. 24, Created)
CC CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC CC DE 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
CC CC DE (BC 1.1.1.31) (HIBADH).
CC CC GN HIBADH.
CC CC OS Rattus norvegicus (Rat).

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OC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC CC NCBI_TaxID=10116;
OC CC
OC CC [1]
OC CC SEQUENCE FROM N.A.
OC CC STRAIN=Sprague-Dawley; TISSUE=Liver;
OC CC MEDLINE=89174651; PubMed=2647728;
OC CC RA Rougaff P.M., Zhang B., Kuntz M.J., Harris R.A., Crabb D.W.;
OC CC "Cloning and sequence analysis of a cDNA for 3-hydroxyisobutyrate
OC CC dehydrogenase. Evidence for its evolutionary relationship to other
OC CC pyridine nucleotide-dependent dehydrogenases.";
OC CC RL J. Biol. Chem. 264:5899-5903 (1989).
OC CC [2]
OC CC MUTAGENESIS.
OC CC MEDLINE=96335606; PubMed=8766712;
OC CC RA Hawes J.W., Harper E.T., Crabb D.W., Harris R.A.;
OC CC "Structural and mechanistic similarities of 6-phosphogluconate and 3-
OC CC hydroxyisobutyrate dehydrogenases reveal a new enzyme family, the 3-
OC CC hydroxyacid dehydrogenases.";
OC CC RL FEBS Lett. 389:263-267 (1996).
OC CC [3]
OC CC CONCEPTUAL TRANSLATION.
OC CC RA Bairoch A.;
OC CC RL Unpublished observations (JAN-2001).
OC CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
OC CC methyl-3-oxopropanoate + NADH.
OC CC -!- SUBUNIT: Homodimer.
OC CC -!- SUBCELLULAR LOCATION: Mitochondrial.
OC CC -!- TISSUE SPECIFICITY: HIGHER LEVEL IN KIDNEY, LIVER, AND HEART THAN
OC CC IN MUSCLE.
OC CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
OC CC family.
OC CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
OC CC frameshift in position 10.
OC CC
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OC CC or send an email to license@isb-sib.ch).
OC CC
OC CC EMBL; J04628; AAA50312.1; ALT_FRAME.
OC CC PIR; A32867; A32867.
OC CC InterPro; IPR002204; 3hydroxisobut_dh.
OC CC InterPro; IPR006183; 6PGD.
OC CC InterPro; IPR006115; 6PGD_NAD.
OC CC Pfam; PF03446; NAD binding 2; 1.
OC CC PRINTS; PR00076; 6PGDHRGNASE.
OC CC PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
OC CC Oxidoreductase; NAD; Mitochondrion. Transit peptide.
OC CC TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).
OC CC CHAIN 36 335 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
OC CC NP_BIND 39 67 NAD (ADP PART) (POTENTIAL).
OC CC ACT_SITE 208 208 PROBABLE.
OC CC MUTAGEN 68 68 D->R: DECREASE OF ACTIVITY WITH NAD,
OC CC INCREASE OF ACTIVITY WITH NADP.
OC CC K->A,H,N,R: COMPLETE LOSS OF ACTIVITY.
OC CC N->Q: DECREASE IN ACTIVITY.
OC CC MUTAGEN 208 208
OC CC MUTAGEN 212 212 N->Q: DECREASE IN ACTIVITY.
OC CC SEQUENCE 335 AA; 35302 MW; D266A7838500295A CRC64;
OC CC
OC CC Query Match 10.1%; Score 290; DB 1; Length 335;
OC CC Best Local Similarity 25.5%; Pred. No. 3e-11;
OC CC Matches 79; Conservative 60; Mismatches 157; Indels 14; Gaps 4;
OC CC
OC CC QY 247 GSTSIQAADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVMNRRTAEKCDLF 306
OC CC Db 25 GSLLAAVCSRSMA---SKTP---VGFGLGNMGNPMKLNKKGYPILLYDFPVDCKEF 77
OC CC
OC CC QY 307 IOEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGSPGVQLGIRPKCYVDMSTVDAD 366
OC CC Db 78 KEAGEQVASSPADVAEKADRIITMLPSSNNAVEVYSGANGILKKVKGSLIDSITDPS 137

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QY	367	TVTELAQVIVSRGGRFLFAPVSGNQQLSNDGMLVILAAGDRLGYEDCSFCFQAMGKTSFF	420
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QY	427	LGEVGNAAKMMLIVNMVQGSFNATTAGTLTAHVTGQSQQTLLDIIN--QGQIASIFLDQ	484
Db	198	CGAVSGGOSAKICNMMLAISMIGTFAEAMNLGIRSLGDPKLLAKLINSSGRCWSDTYN	257
QY	485	KCONILQG-----NFKPDPFLYKIQKRLRLATALGDVAVNHPTPMAAANEVVKRAKALDQ	539
Db	258	PVPGVMDGVPPSNNVQGGFTTLMADKLGLAQDSATSTKTPILLGSAHQIYRMMCSKGY	317
QY	540	SDNDMSAVYR	549
Db	318	SKKOFFSSVFQ	327
RESULT 8			
YIHU_SALTY			
ID	YIHU_SALTY	STANDARD;	PRT; 298 AA.
DT	Q9L7S0;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Hypothetical oxidoreductase Yihu (EC 1.1.-.-).		
GN	YIHU OR STM4023.		
OS	Salmonella typhimurium.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Salmonella.		
NCBI_TaxID=602;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Lr2;		
RA	Krogan N.J., Zhang R., Neuhard J., Kelln R.A.;		
RT	"Utilization of dihydrocrotonate as sole pyrimidine source by Salmonella		
RT	typhimurium."		
RT	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Lr2 / SGSC1412 / ATCC 700720;		
RX	MEDLINE=21534948; PubMed=11677609;		
RA	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,		
RA	Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,		
RA	Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,		
RA	Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,		
RA	Waterston R., Wilson R.K.;		
RT	"Complete genome sequence of Salmonella enterica serovar Typhimurium		
RT	Lr2."		
RL	Nature 413:852-856(2001).		
CC	-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase		
CC	family.		
CC	-----		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
EMBL;	AF220438; AAF27921.1; -;		
DR	EMBL; AE008887; AAL22862.1; -;		
DR	StyGene; SG7???; Yihu		
DR	InterPro; IPR002204; 3hydroxisobut_dh.		
DR	InterPro; IPR061115; 6PGD_NAD.		
DR	InterPro; IPR000205; NAD_BS.		
DR	Pfam; PF03446; NAD_binding_2; 1.		
DR	PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.		
KW	Hypothetical protein; Oxidoreductase; NAD; Complete proteome.		
FT	ACT SITE 171 171 BY SIMILARITY.		
SEQUENCE	298 AA; 31280 MW; 7ED9FA174249240C CRC64;		

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).
RL
RN [2]

RP SEQUENCE OF 37-47.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Rabinovitch A., Rabinovich D., Wochstatter D.F.

CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase family.

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CC or send an email to license@isb-sib.ch).

QY 370 ELAQVIVSGRFLPAPVSGNQLNDGMLVLAAGDRGLYEDCSFCQAMGKTSFFLGE 429
DB 142 ELAKEVERMGAVFMDAPVSGVGAARSGLNLTWVGVEDEFAAAQELLGCMGNSVYVCA 201
QY 430 VGNAAKMLIVNMVQGSFMTATAGTLTAHVTGQSQOQLLDLN--QGQASIFLDQKQC 487
DB 202 VTGQAACINNMILAIISMIGTAEMNGLIRGLDPLKLLAKLINMSSGRCWSSTYNPVP 261
QY 488 NILQ-----NFKPDFYLKVIQDLRLALATGADVNNPTEMAAAANVYKRAKALDQSDN 542
DB 262 GWMDCVPSANNYQGGFTTLMAKDLGLAQDSTATSKSPILLGSLAHQIYRMCAKGYSKK 321
QY 543 DMSAVIR 549
DB 322 DFSSVQF 328

RESULT 11
D3HI_DROME
ID D3HI_DROME STANDARD; PRT; 324 AA.
AC Q9V8M5; Q9V8M6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
DE (EC 1.1.1.31) (HIBADH).
GN CG15093.

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.R., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D.A., Heiman T.J., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
CC methyl-3-oxopropanoate + NADH.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q9V8M5-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q9V8M5-2; Sequence=VSP_001281, VSP_001282;
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC -----

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EMBL; AE003798; AAF57638.2; -;
DR EMBL; AE003798; AAF57638.2; -;
DR FLYBase; FBgn0034390; CG15093.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6FGDHRGNASE.
DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
DR Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;
KW Transmembrane; Alternative splicing.
FT TRANSIT 1 25 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 26 324 PROBABLE 3-HYDROXYISOBUTYRATE
FT NP_BIND 29 57 DEHYDROGENASE.
FT ACT_SITE 196 196 NAD (ADP PART) (POTENTIAL).
FT VARSPPLIC 95 227 BY SIMILARITY.
FT FTId=VSP_001281.
FT Missing (in isoform Short).
FT /FTId=VSP_001282.
SQ SEQUENCE 324 AA; 33883 MW; A39B534753BAE83E CRC64;

Query Match 9.7%; Score 278.5; DB 1; Length 324;
Best Local Similarity 26.5%; Pred. No. 1.5e-10;
Matches 79; Conservative 47; Mismatches 143; Indels 29; Gaps 5;
QY 268 KKTGFTGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFTQEGARLGRTPAEVSTCDIT 327
DB 29 KNIGFVGLGMGAMASNLKAGHKLHVFDISKPADGLAAGKATVYAKTSELAKNSDFV 88
QY 328 FACVSD---PKAAKDLVLGSGVLQIRPGKCYVDMSTVDADTVTTELAQIVISVRGGRFLE 384

Db 89 ITMLPNNNAIVDASDEM-----TADGVNKDTIFIDSSTISPDLYKSLQKTSKARGARID 143
 Qy 385 APVSGNQLSNDGMLVILAAAGDGLYEDSCSCFQAMGKTSFPLGEVGNAAKMLIVNMVQ 444
 Db 144 APVSGVPGACQATLTFWVGTEAEYNAVAVKAVLECMGKKITHCGVYGMQGAQKLCNNMML 203
 Qy 445 GSFMTATIAEGLTLAHVTGQSQTLLDILNQQLASIFLDQKC-----QNILQG----- 492
 Db 204 AISMIGVSEAMNLAVRQGLDANVFABIINS-----TGRCWASEIYNPVPVGVCPSPAPA 256
 Qy 493 --NEKPDYLVYKQDLRLALATGDAVNHPTPMAAAANEVYKRAKALDQSDNMSAVY 548
 Db 257 NRDVAGGFSSALITKDLGLASGVANASNPPLGSLAHKVYQSLCDKGLGNKDFSVVY 314

RESULT 12
 MMSB_PSEAE STANDARD; PRT; 298 AA.
 ID MMSB_PSEAE STANDARD; PRT; 298 AA.
 AC P28811;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH).
 GN MMSB OR PA3569.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=92317087; PubMed=1339433;
 RA Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.;
 RT "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO
 RT encoding methylmalonate-semialdehyde dehydrogenase and 3-
 RT hydroxyisobutyrate dehydrogenase."
 RL J. Biol. Chem. 267:13585-13592(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Harbig K., Lim R.W.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964 (2000).
 RC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
 CC methyl-3-oxopropanoate + NADH.
 CC -!- PATHWAY: Distal valine metabolic pathway.
 CC -!- INDUCTION: By valine.
 CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
 CC family.
 CC
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 CC
 CC EMBL; M84911; AAA25892.1; --
 DR EMBL; AE004778; AAG06957.1; --
 DR PIR; C42902; C42902.
 DR InterPro; IPR002204; 3hydroxisobut_dh.
 DR Pfam; PF03446; NAD binding 2; 1.
 DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.

KW Oxidoreductase; NAD; Complete proteome.
 FT NP_BIND 3 31 NAD (BY SIMILARITY).
 FT ACT_SITE 171 171 BY SIMILARITY.
 SQ SEQUENCE 298 AA; 30486 MW; 0C4D7B5A7C870730 CRC64;
 Query Match 9.1%; Score 261.5; DB 1; Length 298;
 Best Local Similarity 25.8%; Pred. No. 1.6e-09;
 Matches 76; Conservative 51; Mismatches 151; Indels 17; Gaps 4;
 Qy 270 IGFGLGIMSGIYSNLLKMGHTVVMNRTEAKCDLFTQEGARLGRTPAEVVSTCDITFA 329
 Db 4 IAFGLGNMGPMANLLKAGHRVNVFLDKAVLGLIVEQAGQAGDSALQCEGAEEVVIS 63
 Qy 330 CVSPPKAAKDLVLGPGSVLQIRPKCYVMSTVDADTVELAQVIVVGRGGRFLBAPVSG 389
 Db 64 MLPAGQHVESLYLGDGDLARVAGKPLLDICSTIAPTARKVAEAAAAGKGLTLLDAPVSG 123
 Qy 390 NQQLSNDGMVLAAAGDGLYEDSCSCFQAMGKTSFPLGEVGNAAKMLIVNMVGSFMA 449
 Db 124 GVGGARAGTSLFVGGPAGFARAPVLENMGRNIFHAGDHGAGQVAKICNNMLLGILMA 183
 Qy 450 TIAEGLTLAHVTGQSQTLLDILNQ-----GOLA-----SIFLDQKCNILQGNFKPDF 498
 Db 184 GTAEALALGVKNGLDPAVLSEVMKQSSGNNWALNLYNFWPQVMPQAPASNGVAGGFQ--- 240
 Qy 499 YLKYTKDKRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDN--DMSAVTRAY 551
 Db 241 -VRLNKNKDLGLALANAQAQVASTPLGLARNLFSLHAQADAHEGLDFDSIQKLY 294

RESULT 13
 DH31 CAEEL STANDARD; PRT; 299 AA.
 ID DH31 CAEEL STANDARD; PRT; 299 AA.
 AC Q9XTT0.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial
 DE (EC 1.1.1.31) (HIBADH).
 GN B0250.5
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RL Lloyd C., White S.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2-
 CC methyl-3-oxopropanoate + NADH.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
 CC family.
 CC
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 CC
 CC EMBL; Z81453; CAB03798.1; --
 DR EMBL; AL031630; CAB03798.1; JOINED.
 DR EMBL; AL031630; CRA21003.1; --
 DR EMBL; Z81453; CAA21003.1; JOINED.
 DR PIR; T18682; T18682.
 DR WormPep; B0250.5; CE18481.
 DR InterPro; IPR002204; 3hydroxisobut_dh.
 DR PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
 DR Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 KW NP_BIND 2 30 NAD (ADP PART) (POTENTIAL).
 FT


```

FT ACT_SITE 172 172 PROBABLE.
SQ SEQUENCE 299 AA; 31217 MW; F30B423A597CABF0 CRC64;

Query Match
Best Local Similarity 9.1%; Score 259.5; DB 1; Length 299;
Matches 77; Conservative 48; Mismatches 143; Indels 31; Gaps 6;

QY 271 GFLGLGMSGIVSNLLKMGHTVTVNRTAEKDLFIQEGARLGRTPAEVSTCDITFAC 330
DB 5 GFIGLNGMGHMARNLKNKKLIVYDNKAVVQEFKAGCEVAHPADIAAASKEIITV 64

QY 331 VSDPKAAKDLVLPSPGVLOGIRPKCYVDMSTVDADTTELAQVIVSRGRLPAPVSGN 390
DB 65 LPSPGHKAVVQGEAGIFKTIQPGTCLMDSSTIDQIVSLEVAQAAALLKAEYDAPISGG 124

QY 391 ----QQLSNDGMLVILAAGDRLGYEDCSFQAMGKTSFFLGEVGNAAKMWLIVNMGVS 446
DB 125 VTGAQAT--LTPMVGAGNDATFKRAEAVLSLMGKNIVNLGAVNGTAATKCNMLLGI 181

QY 447 FMATIAEGLTIAHVTGSGQQTLDLIN-----QGQIASIFLDKQCNILQ 491
DB 182 QMVAVAETMNLGISMLGDAKALAGIVNTSSRCWSSDTYNVPVGIENI---PSCRGYAG 238

QY 492 GNEKPEVLKVIQKDLRLAIALGDVNHPTMAAAANEVYKRAKALDQSDNDSAVYR 549
DB 239 G-----FGTLLMAKDLSLAQNASTNTQAPTPTMGSLAHQIYRILARDPOYQAKDFGVYQ 292

RESULT 14
YGBJ ECOLI
ID YGBJ ECOLI STANDARD; PRT; 302 AA.
AC Q6888;
DT 15-JUL-1998 (Rel. 36, Created)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase ygbJ (EC 1.1.-.-).
GN YGBJ OR B2736.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
CC
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CC
CC -----
CC ENBL; U29579; AAA69246.1; --
CC DR ENBL; AE000357; AAC75778.1; --
CC DR PIR; D65054; D65054.
CC DR EcoGene; EG13104; ygbJ.
CC DR InterPro; IPR002204; 3hydroxisobut dh.
CC DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
CC KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT ACT_SITE 178 178 BY SIMILARITY
SQ SEQUENCE 302 AA; 30751 MW; 09E94256EDDFC26C CRC64;

Query Match
Best Local Similarity 22.9%; Pred. No. 4.1e-08;
Matches 67; Conservative 64; Mismatches 155; Indels 6; Gaps 4;

QY 264 TPTDKKIGFLGLGMSGIVSNLLKMGHTVTVN--NRTAEKCDLFIQEGA-RLGRTPAEV 320
DB 3 TGSEPHGVIVGLSGMGMAALSYVRAG--LSTWGADLNSNACATLKEAGCGVSDNAATF 60

QY 321 VSTCDITFACVSDPKAAKDLVLPSPGVLOGIRPKCYVDMSTVDADTTELAQVIVSRGG 380
DB 61 AEKLDALLVLVNAQAQVQVLFGETGVAQHLKPGTAVMVSTSIAGADAQEIATALAGFDL 120

QY 381 RFLPAPVSGNQQLSNDGMLVILAAGDRLGYEDCSFQAMGKTSFFLG-EVGNAAKMWLI 439
DB 121 EMLDAPVSGGKAVKANGEMTVWASSDIAFLAPLVAIVAGKVVIRIAGPGLGTVKII 180

QY 440 VNVQGSFMATIAEGLTIAHVTGSGQQTLDLINQGQIASIFLDKQCNILQGNFKPDFY 499
DB 181 HQLLAGVHIAAGAEAMALAARAGIPLDVMDYDVTNNAAGSNWFMNRHVRVDDYTPHSA 240

QY 500 LKVIQKDLRLAIALGDVNHPTMAAAANEVYKRAKALDQSDNDSAVYR 551
DB 241 VDFVVKDLGLVADTAKALHFFPLPLASTALNMFTSASNAGYKGEDDSAVIKIF 292

RESULT 15
MMSB MYCTU
ID MMSB MYCTU STANDARD; PRT; 294 AA.
AC O53814;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH).
GN MMSB OR RV0751C OR MT0775 OR MTU041.25C OR MB0773C.
OS Mycobacterium tuberculosis; and
OS Mycobacterium tuberculosis; and
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RA complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Paterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RA laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

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Db 121 AKPLDLSLQOIFDVCEESTANAAK--ISINFLVSMLEALSESEFLMMKYEKLEQKQFL 178
QY 470 DIINQOLASIFUDKQCN-----ILQNFKP-DFYLYKYQKDLRLAIALGDAVNHPTMA 524
Db 179 EI-----AKALFGSPYVGTITMAEQKPEPAGFKMSLGLKQTNLALAAKRVSANPLA 233
QY 525 AANEVYKRAKALQSDNDMSAVYR 549
Db 234 ELAKSHFESGIEKFGGLDWAALIK 258

RESULT 17
Y770 MYCTU
ID V770 MYCTU STANDARD; PRT; 295 AA.
AC P71825;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase Rv0770/MT0794 (EC 1.1.1.-.-).
GN Rv0770 OR MT0794 OR MTCY369.15.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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Query Match 7.3%; Score 209.5; DB 1; Length 295;
Best Local Similarity 24.7%; Pred. No. 2.8e-06;
Matches 69; Conservative 48; Mismatches 137; Indels 25; Gaps 5;

QY 265 PDKKIGFLGLGMSGIIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTC 324
Db 5 PETPRLYIGLGNQAGAPMAKRLLDWPGGLTVFDRVVEAMAPFVEGGATAASVSD-VAEA 63
QY 325 DITFACVSDPKAAKDLVLGSPVLQGIIRPKGKCYVDMSTVDADTDTVLAQVIVSRGRFLE 384
Db 64 DIISITVFDDAQVSSVITADNGLATHAKPGTIVAHSTIADTTAVDLAEKLPQGIHVD 123
QY 385 APVSGNQQLSNDGMLVILAAGDRLGYEDCCSCFOAMGKTSFPLGEVGNAAKMLIVNMVQ 444
Db 124 APVSGAAAKAGELAVWVGADDEAFQRIKEPFSRWASLLIHAGFPGAGTRMKLARNMLT 183
QY 445 GSFMTIAEGLTIAHVTVGSGSQQLDILNQQL-----ASIFLDKCKCNILQG 492
Db 184 FVSVAAMAEAQRLAEACG-----LDLVALGKVVRHSDSFTGGAGAIMFRNTTAPMEPAD 237
QY 493 NFKDPFYKYI-----QKDLRLAIALGDVNHPTMAAAA 527
Db 238 PLRP--LLEHTRGLGKDLALALGCVVSDPLAQLA 274

RESULT 18
YGBJ HAEIN
ID YGBJ HAEIN STANDARD; PRT; 301 AA.
AC P44979;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase H11010 (EC 1.1.1.-.-).
GN H11010.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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RESULT 19
HDGF MOUSE
ID HDGF MOUSE STANDARD; PRT; 237 AA.
AC P51859; Q9CYA4; Q9JK87;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatoma-derived growth factor (HDGF).
DE HDGF OR TDRM1.
GN HDGF
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;

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RA Izumoto Y., Kuroda T., Harada H., Kishimoto T., Nakamura H.;
 RA Hepatoma-derived growth factor belongs to a gene family in mice
 RT showing significant homology in the amino terminus.";
 RL Biochem. Biophys. Res. Commun. 238:26-32(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RA Zhao Y., Chen W., Wang Y.;
 RT "Cloning of novel gene related to thymus development.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Saito K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Saito K.

RA Fleischnmann W., Gaasterland T., Gassi C.C., King B., Koculuwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Buffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein S.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Guernstein M.

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QY 67 KEEMIKKGRFOQAVDAVEFLRAKQKQTSNHSNDDKRRNSSEERSRPNSGDEK 126
Db 70 KEFTGKPNKRKFSEGLWEIEN-----NPTVKASYQSSQKKSCAAAEPEVEPEAHEGDD 124
QY 127 RKLISLSEKVKKNWEGSKRVSSESSSSESGSKPLKR-----AQOSPRKGRPPK-----D 177
Db 125 KKGS-AEGSSDE--EGKLVIDEPAKNEKNEGTLLKRAAGDVLEDSPKR---PRESGDHE 176
QY 178 EKDLTIPSSVTGMMAGPMAAFKWOPTASBPVKDADP 215
Db 177 EED---KEIAALEGERPLPVEVEK-NSTPSPDGGQP 210

RESULT 20
YCY3 SHEFR
ID YCY3 SHEFR STANDARD; PRT; 194 AA.
AC O33730;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical oxidoreductase in cytochrome c3 5' region (Fragment).
OS Shewanella frigidimarina.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=56812;
RN SEQUENCE FROM N.A.
RC STRAIN=NCIMB 400;
RX PubMed=10861223;
RA Gordon E.H.J., Pike A.D., Hill A.E., Cuthbertson P.M., Chapman S.K.,
RA Reid G.A.;
RT "Identification and characterization of a novel cytochrome c3 from
RT Shewanella frigidimarina that is involved in Fe(III) respiration.";
RL Biochem. J. 349:153-158(2000).
CC -i SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
CC family.
CC
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CC
CC EMBL: AJ000006; CAA03849.1; -
KW Hypothetical protein; Oxidoreductase; NAD.
FT NON_TER
SQ SEQUENCE 194 AA; 20865 MW; 4B4236749F1E8701 CRC64;

Query Match 6.5%; Score 185.5; DB 1; Length 194;
Best Local Similarity 26.3%; Pred. No. 5.2e-05;
Matches 51; Conservative 45; Mismatches 81; Indels 17; Gaps 5;

QY 362 TVDADTVTELAQVIVSRGGRFLEAPVSGNQSLNDGMLVLAAGDRGLYE-----DCSS 415
Db 1 TAGADVAREIAAYEPLNIAFLDAPVSGQAGANGALVTWVGSDQAHFDTVKPVISAYS 60
QY 416 CFQAMGKTSFELGVGNAAKMLIVNMVQGSFMATIAEGLTIAHTVQSQQTLLDILNQG 475
Db 61 CABELLFVG--AGQLTKVNVQICIAGVVQG-----LAEGHFAKSLDGLGVIEVISKG 113
QY 476 QLASIFLDQKONITLQCNFKPDPFVLKYIOKDLRLAIALGADVNHPT--PMAAANAEVYKR 533
Db 114 RAQSQWQENRYKTMQCCQYDFGFAIDWNRKD--LGIALDEARRNGSHLPVAALVDQFYSE 171
QY 534 AKALQSDNDMSAV 547
Db 172 VQAMKGNRWDTSLL 185

RESULT 21
HDGF_HUMAN

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HDGF_HUMAN STANDARD; PRT; 240 AA.
P51858;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatoma-derived growth factor (HDGF) (High-mobility group protein 1-
DE like 2) (HMG-1L2).
GN HDGF OR HMG1L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A., AND SEQUENCE OF 4-24.
RC TISSUE=Hepatoma;
RX MEDLINE=95014294; PubMed=7929202;
RA Nakamura H., Izumoto Y., Kambe H., Kuroda T., Mori T., Kawamura K.,
RA Yamamoto H., Kishimoto T.;
RT "Molecular cloning of complementary DNA for a novel human hepatoma-
RT derived growth factor. Its homology with high mobility group-1
RT protein.";
RL J. Biol. Chem. 269:25143-25149(1994).
RN [2]
RC SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -i FUNCTION: Heparin-binding protein, with mitogenic activity for
CC fibroblasts.
CC -i SUBCELLULAR LOCATION: Cytoplasmic.
CC -i TISSUE SPECIFICITY: Ubiquitous.
CC -i SIMILARITY: Contains 1 PWMP domain.
CC
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CC EMBL: D16431; BAA03903.1; -
DR EMBL; BC018991; AH18991.1; -
DR PIR; A55055; A55055.
DR Genew; HGNC:4856; HDGF.
DR MIM; 300043; -
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0005615; Extracellular space; TAS.
DR GO; GO:0008201; Heparin binding; TAS.
DR GO; GO:0008283; P-cell proliferation; TAS.
DR InterPro; IPR000313; PWMP_domain.
DR Pfam; PF00855; PWMP; 1.
DR SMART; SM00293; PWMP; 1.
DR PROSITE; PS50812; PWMP; 1.

```

RT "Molecular cloning of the N-terminus of GTPBP.";
RL Genomics 31:395-397(1996).
RN [6]
RX CHARACTERIZATION, AND PARTIAL SEQUENCE.
RP MEDLINE=95327933; PubMed=7604264;
RA Drummond J.T., Li G.-M., Longley M.J., Modrich P.;
RT "Isolation of an hMSH2-p160 heterodimer that restores DNA mismatch
RT repair to tumor cells.";
RL Science 268:1909-1912(1995).
RN [7]
RN IDENTIFICATION OF MSH6 AS MEMBER OF BASC.
RX MEDLINE=20245492; PubMed=10783165;
RA Wang Y., Cortez D., Yazdi P., Neff N., Ellledge S.J., Qin J.;
RT "BASC, a super complex of BRCA1-associated proteins involved in the
RT recognition and repair of aberrant DNA structures.";
RL Genes Dev. 14:927-939(2000).
RN [8]
RN DISEASE.
RX MEDLINE=98016406; PubMed=9354786;
RA Miyaki M., Konishi M., Tanaka K., Kikuchi-Yanoshita R., Muraoka M.,
RA Yasuno M., Igari T., Koike M., Chiba M., Mori T.;
RT "Germline mutation of MSH6 as the cause of hereditary nonpolyposis
RT colorectal cancer.";
RL Nat. Genet. 17:271-272(1997).
RN [9]
RN VARIANTS VAL-1213 AND ILE-1260.
RX MEDLINE=95327935; PubMed=7604266;
RA Papadopoulos N., Nicolaides N.C., Liu B., Parsons R., Lengauer C.,
RA Palombo F., D'Arrigo A., Markowitz S., Willson J.K.V., Kinzler K.W.,
RA Jiricny J., Vogelstein B.;
RT "Mutations of GTPBP in genetically unstable cells.";
RL Science 268:1915-1917(1995).
RN [10]
RN VARIANTS HNPPC5 ILE-144 AND CYS-850.
RX MEDLINE=99452590; PubMed=10521294;
RA Wu Y., Berends M.J.W., Mensink R.G.J., Kempinga C., Sijmons R.H.,
RA van Der Zee A.G.J., Hollma H., Kleibeker J.H., Buys C.H.C.M.,
RA Hofstra R.M.W.;
RT "Association of hereditary nonpolyposis colorectal cancer-related
RT tumors displaying low microsatellite instability with MSH6 germline
RT mutations.";
RL Am. J. Hum. Genet. 65:1291-1298(1999).
RN [11]
RN VARIANTS CRC ILE-285; ARG-566; GLY-803 AND THR-1087, AND VARIANTS
RX GLY-39; ASP-220; VAL-396 AND LEU-800.
RP MEDLINE=20050667; PubMed=10537275;
RA Kolodner R.D., Tytell J.D., Schmeits J.L., Kane M.F., Gupta R.D.,
RA Weger J., Wahlberg S., Fox E.A., Peel D., Ziogas A., Garber J.E.,
RA Syngal S., Anton-Culver H., Li F.P.;
RT "Germline msh6 mutations in colorectal cancer families.";
RL Cancer Res. 59:5068-5074(1999).
RN [12]
RN VARIANT HNPPC5 GLU-698.
RX MEDLINE=99408236; PubMed=10480359;
RA Wang Q., Lasset C., Desseigne F., Saurin J.-C., Maugard C.,
RA Navarro C., Ruano E., Descos L., Trillet-Lenoir V., Bosset J.-F.,
RA Puisieux A.;
RT "Prevalence of germline mutations of hMLH1, hMSH2, hPMS1, hPMS2, and
RT hMSH6 genes in 75 French kindreds with nonpolyposis colorectal
RT cancer.";
RL Hum. Genet. 105:79-85(1999).
RN [13]
RN VARIANT HNPPC5 ALA-878.
RX MEDLINE=21470348; PubMed=11586295;
RA Wu Y., Berends M.J.W., Sijmons R.H., Mensink R.G.J., Verling E.,
RA Kooi K.A., van der Sluis T., Kempinga C., van der Zee A.G.J.,
RA Hollma H., Buys C.H.C.M., Kleibeker J.H., Hofstra R.M.W.;
RT "A role for MLH3 in hereditary nonpolyposis colorectal cancer.";
RL Nat. Genet. 29:137-138(2001).
RN [14]
RN VARIANT CRC HIS-976.
RX MEDLINE=21666030; PubMed=11807791;
RA Plaschke J., Krueger S., Fistorius S., Theissig F., Saeger H.D.,
RA

KW Growth factor; Heparin-binding.
FT DOMAIN 12 69 PWWP.
FT DOMAIN 213 223 POLY-GLU.
SQ SEQUENCE 240 AA; 26788 MW; DD60D9203BDD4B34 CRC64;
Query Match 6.5%; Score 185.5; DB 1; Length 240;
Best Local Similarity 29.8%; Pred. No. 6.8e-05;
Matches 64; Conservative 30; Mismatches 100; Indels 21; Gaps 8;
QY 7 RLGDVWGKLGYPWPFGKIVNPPKDLKPRGKKCFVFGTDEHAWIKVEQLKPYHAH 66
DB 11 KCGDLVPKMKGVHPNPARIDEMEAVKATANK-YQVFFGTHETAFGLPKOLFPEES 69
QY 67 KEEMIKINKGRFQQAQDAVEEFLRAKGDQTSNHSDDKXNRNSESERSRPNSGDEK 126
DB 70 KEKFGKFNKRGKRGSEGLWEIEN-----NPTVKASGYQSSQKSCVERPEPEAAEGDGD 124
QY 127 RKLSLSEGVKKNGKGEKRVSSSSSRRGSKSPKRAQ-----EQSPR--KRGPPKDEKD 180
DB 125 KK-GNAEGSSDE---EGLVIDEPAKNEKGALKRRAGDLLEDSPKPKAEANPEGEE- 179
QY 181 LTIPESTVTKGMAGPMAAFKMQQTASEPVKQADP 215
DB 180 ---KEAATLEVERPLMEVEK-NSTPSEPGSGRGP 210
RESULT 22
MSH6 HUMAN
ID -MSH6_HUMAN STANDARD; PRT; 1360 AA.
AC P52701; Q43706; Q43917; Q8TCX4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA mismatch repair protein MSH6 (Muts-alpha 160 kDa subunit) (G/T
DE mismatch binding protein) (GTPBP) (GTMBP) (P160).
GN MSH6 OR GTPBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97098445; PubMed=8942985;
RA Acharya S., Wilson T., Gradia S., Kane M.F., Guerrette S.,
RA Matischky G.T., Kolodner R.D., Fishel R.;
RT "MSH2 forms specific mismatch-binding complexes with hMSH3 and
RT hMSH6.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13629-13634(1996).
RN [2]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=98116665; PubMed=9455487;
RA Shiwaku H.O., Wakatani S., Mori Y., Fukushima S., Horii A.;
RT "Alternative splicing of GTPBP in normal human tissues.";
RL DNA Res. 4:359-362(1997).
RN [3]
RN SEQUENCE FROM N.A., AND VARIANT GLY-39.
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,
RA Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 69-1360 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95327934; PubMed=7604265;
RA Palombo F., Gallinari P., Iaccarino I., Lettieri T., Hughes M.,
RA D'Arrigo A., Truong O., Hsuan J.J., Jiricny J.,
RT "GTPBP, a 160-kilodalton protein essential for mismatch-binding
RT activity in human cells.";
RL Science 268:1912-1914(1995).
RN [5]
RN SEQUENCE OF 1-116 FROM N.A., AND VARIANT GLY-39.
RX MEDLINE=98435440; PubMed=893826;
RA Nicolaides N.C., Palombo F., Kinzler K.W., Vogelstein B.,
RA Jiricny J.;

Schackert H. K.;
 "Involvement of hMSH6 in the development of hereditary and sporadic colorectal cancer revealed by immunostaining is based on germline mutations, but rarely on somatic inactivation.";
 Int. J. Cancer 97:643-648(2002).
 -!- FUNCTION: Restores repair of base-base and single- nucleotide insertion-deletion mismatches, and increases the proficiency to process heteroduplexes with two-, three-, or four- nucleotide insertion-deletion mismatches. GTBP binds covalently to G/T mismatches.
 -!- SUBUNIT: Heterodimer of MSH2 and MSH6 (GTBP). Part of the BRCA1-associated genome surveillance complex (BASC), which contains BRCA1, MSH2, MSH6, MLH1, ATM, BLM, PMS2 and the RAD50-MRE11-NBS1 protein complex. This association could be a dynamic process changing throughout the cell cycle and within subnuclear domains.
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=GTBP-N;
 IsoId=P52701-1; Sequences=Displayed;
 Name=GTBP-alt;
 IsoId=P52701-2; Sequences=VSP_003291, VSP_003292;
 -!- PTM: The N-terminus is blocked
 -!- DISEASE: Defects in MSH6 are the cause of hereditary non-polyposis colorectal cancer type 5 (HNPCC5) [MIM:60678]. Mutations in more than one gene locus can be involved alone or in combination in the production of the HNPCC phenotype (also called Lynch syndrome). Most families with clinically recognized HNPCC have mutations in either MLH1 or MSH2 genes. HNPCC is an autosomal, dominantly inherited disease associated with marked increase in cancer susceptibility. It is characterized by a familial predisposition to early onset colorectal carcinoma (CRC) and extra-colonic cancers of the gastrointestinal, urological and female reproductive tracts. HNPCC is reported to be the most common form of inherited colorectal cancer in the Western world. Cancers in HNPCC originate within benign neoplastic polyps termed adenomas. Clinically, HNPCC is often divided into two subgroups. Type I: hereditary predisposition to colorectal cancer, a young age of onset, and carcinoma observed in the proximal colon. Type II: patients have an increased risk for cancers in certain tissues such as the uterus, ovary, breast, stomach, small intestine, skin, and larynx in addition to the colon. Diagnosis of classical HNPCC is based on the Amsterdam criteria: 3 or more relatives affected by colorectal cancer, one a first degree relative of the other two; 2 or more generation affected; 1 or more colorectal cancers presenting before 50 years of age; exclusion of hereditary polyposis syndromes. MSH6 mutations appear to be associated with atypical HNPCC and in particular with development of endometrial carcinoma or atypical endometrial hyperplasia, the presumed precursor of endometrial cancer. Defects in MSH6 are also found in familial colorectal cancers (suspected or incomplete HNPCC) that do not fulfill the Amsterdam criteria for HNPCC.
 -!- DISEASE: Defects in MSH6 are a cause of susceptibility to endometrial cancer [MIM:608089].
 -!- SIMILARITY: Belongs to the DNA mismatch repair mutS family.
 -!- SIMILARITY: Contains 1 PWWP domain.
 -!- DATABASES: NAME=Hereditary non-polyposis colorectal cancer db; WWW="http://www.nfcdt.nl/".

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 EMBL; U73737; AAB47425.1; -
 DR EMBL; U73732; AAB47425.1; JOINED.
 DR EMBL; U73733; AAB47425.1; JOINED.
 DR EMBL; U73734; AAB47425.1; JOINED.
 DR EMBL; U73736; AAB47425.1; JOINED.
 DR EMBL; D89645; BAA23674.1; -

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O9:K30:H12 / E69;
 RX MEDLINE=94252978; PubMed=7515042;
 RA Jayaratne P., Bronner D., MacLachlan R.P., Dodgson C., Kido N.,
 RA Whitfield C.;
 RT "Cloning and analysis of duplicated rfbM and rfbK genes involved in
 RT the formation of GDP-mannose in Escherichia coli O9:K30 and
 RT participation of rfb genes in the synthesis of the group I K30
 RT capsular polysaccharide.";
 RL J. Bacteriol. 176:3126-3139(1994).
 CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
 CC 5-phosphate + CO(2) + NADPH.
 CC -!- PATHWAY: Hexose monophosphate shunt.
 CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
 CC family.
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 CC
 DR EMBL; L27646; AAA21136.1; --
 DR F01; 141250; 141250.
 DR HSP; P00349; 2PGD.
 DR InterPro; IPR008927; 6GDH_C-like.
 DR InterPro; IPR006183; 6PGD.
 DR InterPro; IPR006114; 6PGD C.
 DR InterPro; IPR006113; 6PGD decarbox.
 DR InterPro; IPR006115; 6PGD_NAD.
 DR InterPro; IPR006184; 6PGD_BS.
 DR Pfam; PF03933; 6PGD; 1.
 DR Pfam; PF03446; NAD binding 2; 1.
 DR PRINTS; PR00076; 6PGDHDRGNASE.
 DR TIGRfam; TIGR00873; gnd; 1.
 DR PROSITE; PS00461; 6PGD; 1.
 DR Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
 KW SEQUENCE 468 AA; 51625 MW; C13D94CFD78BFF3A CRC64;
 SQ
 Query Match 5.1%; Score 146; DB 1; Length 468;
 Best Local Similarity 22.7%; Pred. No. 0.049;
 Matches 73; Conservative 51; Mismatches 104; Indels 94; Gaps 14;
 QY 268 KXIFGLGLMGSGIVSNLLKMGHTVTVWNRATKCDLFTQE--GRL--GRTPAEVVST 323
 DB 4 QQIGVGMVAGRNALNIESRGYTVSVFNRSEKTEVIAENPGKKLVPPYTVQEEVES 63
 QY 324 CDITFACVSPKAAKDLVLPSPVLOGIRPGCKVDVMTVDADVTTELAAQVIVSRGRFL 383
 DB 64 -----LETFRILLVMKAGSGTDSALSLKPYLDK-----GILLDGGNTFF 105
 QY 384 EAPVSGNQQLSNDGMLVI---LAAGDRG-----LYED 412
 DB 106 QDITRNRELSAEGFNFIPTGVSAGEGALKGPSIMPGGQKEAYELVAPILKQIAAAVED 165
 QY 413 CSSCFQAMGKTSFPLGEVGNAAKMLVNNVQGSFMATIAE-----GLTLAHTGSGQ 465
 DB 166 GPCVPT-----YIGADGAGHYKVMVNGHIEYGDMLIAYALLKGLTLISN--BELA 216
 QY 466 QTLIDLNOGLASIFLDQKCONILOQNF-KPDEVLYKIQKDLRLAIALGDAVNHP--- 521
 DB 217 QTFTF-WNEGEUSVLYD-----ITKDLFTKDEEGKYL-----VDVILDEAANKGTGK 265
 QY 522 -----PMAAANEVYKR 533
 DB 266 TSQSLDLGLPELSLITESVFR 287

RESULT 24

MSH6 MOUSE
 ID MSH6_MOUSE STANDARD; PRT; 1358 AA.
 AC P54276; O54710;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA mismatch repair protein MSH6 (Muts-alpha 160 kDa subunit) (G/T
 DE mismatch binding protein) (GTBP) (GTMBP) (P160).
 DE MSH6 OR GTMBP.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96411686; PubMed=8812455;
 RA Corradi A., Croci L., Stayton C.L., Gulisano M., Boncinelli E.,
 RA Gonzalez G.G.;
 RT "cDNA sequence, map, and expression of the murine homolog of GTBP, a
 RT DNA mismatch repair gene.";
 RL Genomics 36:288-295(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola;
 RX MEDLINE=98050922; PubMed=9390556;
 RA Edelmann W., Yang K., Umar A., Heyer J., Lau K., Fan K., Liedtke W.,
 RA Cohen P., Kane M.K., Lipford J.R., Yu N., Crouse G.F., Pollard J.W.,
 RA Kunkel T., Lipkin M., Kolodner R., Kucherlapati R.;
 RT "Mutation in the mismatch repair gene Msh6 causes cancer
 RT susceptibility.";
 RL Cell 91:467-477(1997).
 RN [3]
 RP SEQUENCE OF 375-425 AND 1001-1050 FROM N.A.
 RA Donohue P.J., Feng S.H.Y., Alberts G.F., Guo Y., Peifley K.A.,
 RA Hsu D.K.W., Winkles J.A.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Restores repair of base-base and single-nucleotide
 CC insertion-deletion mismatches, and increases the proficiency to
 CC process heteroduplexes with two-, three-, or four-nucleotide
 CC insertion-deletion mismatches. GTBP binds covalently to G/T
 CC mismatches.
 CC -!- SUBUNIT: Heterodimer of MSH2 and MSH6 (GTBP).
 CC -!- SIMILARITY: Belongs to the DNA mismatch repair muts family.
 CC -!- SIMILARITY: Contains 1 PWWP domain.
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 CC
 DR EMBL; U42190; AAC53034.1; --
 DR EMBL; AF031087; AAB88445.1; --
 DR EMBL; AF031085; AAB88445.1; JOINED.
 DR EMBL; AF031086; AAB88445.1; JOINED.
 DR EMBL; U61388; AAB39930.1; --
 DR EMBL; U61389; AAB39931.1; --
 DR MGD; MGI:1343961; Msh6.
 DR InterPro; IPR000432; Muts C.
 DR InterPro; IPR007860; Muts II.
 DR InterPro; IPR007696; Muts III.
 DR InterPro; IPR007861; Muts IV.
 DR InterPro; IPR007695; Muts N.
 DR InterPro; IPR000313; PWWP domain.
 DR Pfam; PF01624; Muts_I; 1.
 DR Pfam; PF05188; Muts_II; 1.
 DR Pfam; PF05192; Muts_III; 1.
 DR Pfam; PF05190; Muts_IV; 1.
 DR Pfam; PF00488; Muts_V; 1.


```

RT "Intergenic transfer and recombination of the 6-phosphogluconate
RT dehydrogenase gene (gnd) in enteric bacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231 (1994).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D21242; BAA04786.1; -
DR EMBL; U14471; AAC43817.1; -
DR PIR; D56146; D56146.
DR HSP; P00349; 2PGD.
DR InterPro; IPR008927; 6GDGH_C_like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD-decarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6EGDHDGRNASE.
DR TIGRfams; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
FT CONFLICT 316 316 G -> E (IN REF. 2).
FT CONFLICT 421 421 V -> F (IN REF. 2).
SQ SEQUENCE 468 AA; 51328 MW; FF1EB5E765FDC90 CRC64;

Query Match 4.9%; Score 141; DB 1; Length 468;
Best Local Similarity 21.4%; Pred. No. 0.1;
Matches 68; Conservative 51; Mismatches 113; Indels 86; Gaps 12;

QY 268 KKGFLGLGMSGIVSNLLKMGHTVTVMNRATKCDLFTQCARLGRTPAEIVVSTCDIT 327
DB 4 QQLGVGVAMVGNRLALNTESRGTYTVSVNRSREKTEEVIAENTGKLPYTVQV--F 60

QY 328 FACVSDPKAAKDLVGPVQGIKPGKCYVMSTVDVDTVELAGVIVSRGGRFLEAPV 387
DB 61 VESLETPRILLVMKAGAGTDSALDSILKPYLDK-----GDIIIDGGNTFFQDTI 109

QY 388 SGNQQLSNDQMLVI---LAAGDRG-----LYEDCSSC 416
DB 110 RNRNRLSAEFGNFIPTGVSGGEGALKGPSIMPGQKEAYELVAPILKQIAVAEAGEPC 169

QY 417 FQAMGKTSFPLGVEGNAAKMLLWVNVQGSFMATIAE-----GLTLARHTVQSQQTLL 469
DB 170 VT-----YIGADGAGHYVMVHNGIEYGDMLIAEYALLKGLALS--BELAQTTT 220

QY 470 DILNQQLASIFLDKQNTLOQNF-KPDPYLKVIQKDLRLALALGDVNVHPT----- 521
DB 221 E-WNEGELSYLID-----ITKDIPTKKDEGKYL-----VDVILDEAANKGTRKTSQS 269

QY 522 -----PMAAANEVYKR 533
DB 270 SLDLGEPLSLITESVFAR 287

RESULT 27
ID -6PGD_SCHPO STANDARD; PRT; 492 AA.
AC P78812; Q9UQW5;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN SPBC660.16.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshiooka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Cabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC -----
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CC -----
DR EMBL; D89161; BAA13823.1; ALT_INIT.
DR EMBL; AL034563; CAA22536.1; -.
DR PIR; T40628; T40628.
DR HSP; P00349; 2PGD.
DR GenDB SPombe; SPBC660.16; -.
DR InterPro; IPR008927; 6GDGH_C_like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD-decarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR006184; 6PGDm_BS.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6EGDHDGRNASE.

```

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DR TIGRFAMS; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Oxidoreductase; Pentose shunt; NADP.
FT CONFLICT 219 220 IA -> ST (IN REF. 1).
SQ SEQUENCE 492 AA; 53679 MW; F55F342957A9D3E1 CRC64;

Query Match
Best Local Similarity 4.8%; Score 138.5; DB 1; Length 492;
Matches 68; Conservative 53; Mismatches 127; Indels 49; Gaps 12;

QY 271 GFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPA-----EVSVC 324
Db 10 GLIGLAVNGQNLINGADKGFTVCYCNRTTSRVDFLANEAK-GKSIIVGAHSLEEFVSKL 68

QY 325 DITFACVSDPKAAKDLVLGSPGVLOGIRP-----GKCYVDMSTVDADTVELAQIVSRGG 380
Db 69 KKPVCILLVRAGKV-----DYLIEGLAPLLEKGDIIIVDGNSHVPTDTRCEEELAKGI 124

QY 381 RPLAPVSGNQLSNDGMVLVLAAGDRGLYEDCSFCQAMGKTS-----FFLGEVGN 433
Db 125 LFGVSGVSGGEGARYGP-SLMPGNGPAAPRIKPIFOTLAAKAGNNEPCCDWCEQAG 183

QY 434 AKMMLIVNVQGSFMATIAE-----GLTLAHTVGSQQTLLDL-----NQQLASIFLD 483
Db 184 HYVMVHNGIYEGDMQLICETVYDMKRGU-----GMSCEADVFEKWNTEKGLDS-FLI 236

QY 484 QKQNILQGNFKPDPFLYKIQDLRLALALG-----DAVNHPTPMAAANEVYKR 533
Db 237 EITRDVLR--YKADGKPLVEKILLDAAGQKGTGKTAQNALEMGTPVSLITEAVFAR 291

RESULT 28
ID 6PGD SHIFL STANDARD; PRT; 468 AA.
AC P37756;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND OR SF2091 OR S2212.
OS Shigella flexneri
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PE577 / Serotype 2a;
RX MEDLINE=94131953; PubMed=7507920;
RA Morona R., Mavris M., Fallarino A., Manning P.A.;
RT "Characterization of the rfc region of Shigella flexneri.";
RL J. Bacteriol. 176:733-747(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T / Arcc 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
```

RESULT 29

```

RL Infect. Immun. 71:2775-2786(2003).
RN [4]
RP SEQUENCE OF 12-456 FROM N.A.
RC STRAIN=ATCC 29903;
RX MEDLINE=95024018; PubMed=7937867;
RA Nelson K., Sclander R.K.;
RT "intergeneric transfer and recombination of the 6-phosphogluconate
RT dehydrogenase gene (gnd) in enteric bacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
CC -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
CC 5-phosphate + CO(2) + NADPH.
CC -!- PATHWAY: Hexose monophosphate shunt.
CC -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
CC family.
CC
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CC
CC EMBL; X71970; CAA50781.1; -.
DR EMBL; AE015225; AAN43630.1; -.
DR EMBL; AE016985; AAP17458.1; -.
DR EMBL; U14468; AAC43834.1; -.
DR HSSP; P00349; 2PGD.
DR InterPro; IPR008927; 6PGDH_C like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD-decarbox.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR006184; 6PGDm_BS.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR TIGRFAMS; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
SQ SEQUENCE 468 AA; 51344 MW; 2203A0D82120CD61 CRC64;

Query Match 4.8%; Score 137; DB 1; Length 468;
Best Local Similarity 20.7%; Pred. No. 0.18;
Matches 68; Conservative 54; Mismatches 100; Indels 106; Gaps 14;

QY 268 KKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPA-EVSVC 323
Db 4 QQIGVGVMAVNGRNALNIERSGYTVSIFNRSREKTEVIAENPKKLAIFYTVKEFVES 63

QY 324 CDITFACVSDPKAAKDLVLGSPGVLOGIRPFGKCYVDMSTVDADTVELAQIVSRGRFL 383
Db 64 -----LETPRILLMVKAGATDAALDSLKPYLK-----GDIIDGNTFF 105

QY 384 EAPVSGNQQLSNDGMVLV-----LAAGDRG-----LYED 412
Db 106 QDITRRNRELSAEGFNFGTGVSGGEGALKGSPMGQKEAYELVAPILTKIAA-VAED 165

QY 413 CSSCFQAMGKTSFPLGEVGNAAKMLIVNVQGSFMATIAE-----GLTLAHTVGSQ 465
Db 166 GEPVCT-----YIGADGAGHYVVMVHNGIEYVDMQMLIAEYSLKGLNLSN--BELA 216

QY 466 QTLDLINQQLASIFLD-----QKQNILQGNFKPDPFLYKIQDLRLALALGDAVN 518
Db 217 QTTFE-WNGELSSYLIDITKDIFTKDED--GNVLVD-----VILDEAN 259

QY 519 HPT-----PMAAANEVYKR 533
Db 260 KGTGKWTQSALDGLGEPLSLITESVFAR 287
```

6PGD_ECOLI
ID _6PGD_ECOLI STANDARD; PRT; 468 AA.
AC P00350; P78080;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GN GND OR B2029.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84237540; PubMed=63299905;
RA Nasoff M.S., Baker H.V. II, Wolf R.E. Jr.;
RT "DNA sequence of the Escherichia coli gene, gnd, for
6-phosphogluconate dehydrogenase";
RL Gene 27:253-264(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12.
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-125 FROM N.A.
RX MEDLINE=89126937; PubMed=2464736;
RA Miller R.D., Dykhuizen D.E., Hartl D.L.;
RT "Fitness effects of a deletion mutation increasing transcription of
the 6-phosphogluconate dehydrogenase gene in Escherichia coli.";
RL Mol. Biol. Evol. 5:691-703(1988).
RN [5]
RP SEQUENCE OF 1-125 FROM N.A.
RX MEDLINE=88086897; PubMed=3275621;
RA Barcak G.J., Wolf R.E. Jr.;
RT "Comparative nucleotide sequence analysis of growth-rate-regulated
gnd alleles from natural isolates of Escherichia coli and from
Salmonella typhimurium LT-2";
RL J. Bacteriol. 170:372-379(1988).
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
CC -1- PATHWAY: Hexose monophosphate shunt.
CC -1- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
family.
CC
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CC
CC EMBL; K02072; AAA23918.1; -.
CC EMBL; AE000294; AAC75090.1; -.

DR EMBL; D90841; BAA15869.1; -.
DR EMBL; M23181; AAA23924.1; -.
DR EMBL; M18956; AAA23919.1; -.
DR EMBL; M18957; AAA23920.1; -.
DR EMBL; M18960; AAA23922.1; -.
DR PIR; D64968; DEECGC.
DR HSSP; P00349; 2PGD.
DR ECOSDBASE; C042.6; 6TH EDITION.
DR EcoGene; EG10411; gnd.
DR InterPro; IPR008927; 6GDH_C-like.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006114; 6PGD_C.
DR InterPro; IPR006113; 6PGD decarbox.
DR InterPro; IPR006115; 6PGD NAD.
DR InterPro; IPR006184; 6PGDm_BS.
DR Pfam; PF00393; 6PGD; 1.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
DR TIGRFAMs; TIGR00873; gnd; 1.
DR PROSITE; PS00461; 6PGD; 1.
KW Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
KW Complete proteome.
FT CONFLICT 306 P -> R (IN REF. 1).
SQ SEQUENCE 468 AA; 51481 MW; 62A32C84DC596D86 CRC64;

Query Match 4.7%; Score 136; DB 1; Length 468;
Best Local Similarity 20.0%; Pred. No. 0.21;
Matches 65; Conservative 54; Mismatches 106; Indels 100; Gaps 12;

QY 268 KKIGFLGLMGSGIVSNLLKMGHTVWNRTEAKCDLFIQE--GARL--GRTPAEVST 323
DB 4 QQIGVGVMAVMGRNLALNIESRGYTVSIFNRSEKTEEVIAENPGKKLVFYTVKRFVS 63

QY 324 CDITFACVSDPKAAKDLVGLPSGVQLGIRPGKYVDMSVTDADTVTELAAQVIVSRGRFL 383
DB 64 -----LETPRILLMVKAGAGTDAIDSLPYLDK-----GDIIDGNTFF 105

QY 384 EAPVSGNQOLSNDGMLVI---LAAGDRG-----LYED 412
DB 106 QDITRRNRELSAEGNFICTGVSGEGALKGPSIMPGQKBEAYELVAPILTAKIAVAED 165

QY 413 CSSCFQAMGKTSFFLGEVGNAAKMLIVNVQSGFMATIAEGLTL-----AHVTGQSQQL 468
DB 166 GEPCVT-----YIGADGAGHYVVMVHNGIEYDMLIAEAYSLLKGLNLNEELAQ 218

QY 469 LDINOGQLASIFLD-----QKONILQGNFKPDFYLYKIQKDLRLAIALGDAVNHPT 521
DB 219 FTEWNGELSSVLIIDITKDIPTKKDED---GNVLVD-----VILDEAANKGT 262

QY 522 -----PMAAANEVYKR 533
DB 263 GKWTSQSALDLGFLSLITESVFAR 287

RESULT 30
MES4 DROME STANDARD; PRT; 1427 AA.
ID MES4 DROME Q8MT36; Q9VAY5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Potential histone methyltransferase Mes-4 (Maternal-effect sterile 4).
GN MES-4 OR CG4976.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balwani R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiland T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP REVISIONS.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnick S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Embryo;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R.A., Gonzalez M., Guarini H., Kroumiller B., Li P.W., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
 RA Celisner S.E.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Potential histone methyltransferase. Histone methylation
 CC gives specific tags for epigenetic transcriptional activation or
 CC repression (by similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: Contains 3 PHD-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 post-SET domain.
 CC -!- SIMILARITY: Contains 2 PWWP domains.
 CC -!- SIMILARITY: Contains 1 SET domain.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 348.
 CC
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 CC
 CC -----
 DR EMBL; AE003763; AAF56762.2; -;
 DR EMBL; AY118404; AAM48433.1; ALT_FRAME.
 DR FlyBase; FBGN0039559; Mes-4.
 DR GO; GO:0000228; C:nuclear chromosome; ISS.
 DR GO; GO:0042054; F:histone methyltransferase activity; ISS.
 DR GO; GO:0016458; P:gene silencing; ISS.
 DR GO; GO:0018992; P:germ-line sex determination; ISS.
 DR InterPro; IPR006560; AWS.
 DR InterPro; IPR003616; PostSET.
 DR InterPro; IPR000313; PWWP_domain.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF00628; PHD; 1.
 DR Pfam; PF00855; PWWP; 1.
 DR Pfam; PF00856; SET; 1.
 DR SMART; SM00570; AWS; 1.
 DR SMART; SM00249; PHD; 3.
 DR SMART; SM00293; PWWP; 2.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS00868; POST_SET; 1.
 DR PROSITE; PS00812; PWWP_2.
 DR PROSITE; PS0280; SET; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 1.
 DR PROSITE; PS0016; ZF_PHD_2; 1.
 KW Nuclear protein; zinc-finger; Metal-binding; Repeat.
 FT DOMAIN 395 468 PWWP 1.
 FT ZN_FING 777 862 PHD-TYPE 1.
 FT ZN_FING 864 932 PHD-TYPE 2.
 FT ZN_FING 999 1044 PWWP 2.
 FT DOMAIN 1049 1111 SET.
 FT DOMAIN 1233 1355 POST-SET.
 FT DOMAIN 1359 1375 POLY-GLN.
 FT DOMAIN 95 100 POLY-GLY.
 FT DOMAIN 174 181
 SQ SEQUENCE 1427 AA; 159027 MW; FB6EFD62E814BEF3 CRC64;
 Query Match 4.7%; Score 135.5; DB 1; Length 1427;
 Best Local Similarity 30.7%; Pred. No. 0.98;
 Matches 35; Conservative 16; Mismatches 40; Indels 23; Gaps 5;
 QY 9 GDVWVGKLGYPWPWPGKIVNPKD-----LKKPRGKCKFFVKFFGTEDHAIKVEQLKPY 63
 Db 1050 GEIVWAKFNFRWPA-IILPPTTEVPNLIKKAHGENDFVVRFFGTHDGHGWSRRVLY 1108
 QY 64 -----HAHKEEMIKINKKFKQAVDAVEFLR-----RAKGDQDTSSHNSD 106
 Db 1109 IEGTGTGCHK-----TKSFLRNYTTGVEASRFLPIIKARQEQDMEROSGN 1156
 Search completed: September 16, 2004, 07:30:47
 Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:28:53 ; Search time 48 Seconds
(without alignments)
3635.033 Million cell upda

Title: US-10-067-482-2

Perfect score: 2866

Sequence: 1 MAAVSLRLGDLVWGKLGYP.....AKALDQSDNDMSAVRAYIH 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Process	Minimum Match	Maximum Match
100% Processing	0%	100%

Listing first 100 summaries

Database :

- ```

1: sp_archea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID     | Description         |
|------------|--------|-------------|--------|----|--------|---------------------|
| 1          | 2811   | 98.1        | 547    | 1  | Q9BXK2 | Q9bxk2 homo sapien  |
| 2          | 2767.5 | 96.6        | 546    | 11 | Q322p9 | Q322p9 mus musculus |
| 3          | 2745.5 | 95.8        | 545    | 11 | Q9CYQ1 | Q9cyq1 mus musculu  |
| 4          | 2683.5 | 93.6        | 523    | 4  | Q9BT11 | Q9bt11 homo sapien  |
| 5          | 796.5  | 27.8        | 602    | 5  | Q8T079 | Q8t079 drosophila   |
| 6          | 727    | 25.4        | 293    | 10 | Q84VC8 | Q84vc8 oryza sativ  |
| 7          | 697    | 24.3        | 289    | 10 | Q94B07 | Q94b07 arabidopsis  |
| 8          | 695    | 24.2        | 289    | 10 | Q9LSV0 | Q9lsv0 arabidopsis  |
| 9          | 667    | 23.3        | 343    | 10 | Q9RWF1 | Q9rwf1 arabidopsis  |
| 10         | 644    | 22.5        | 387    | 10 | Q9LNP0 | Q9lnp0 arabidopsis  |
| 11         | 562    | 19.6        | 248    | 10 | Q94A74 | Q94a74 arabidopsis  |
| 12         | 560    | 19.5        | 343    | 10 | Q8LQJ7 | Q8lqj7 oryza sativ  |
| 13         | 397    | 13.9        | 300    | 17 | Q8RT25 | Q8rt25 methanosaar  |
| 14         | 392.5  | 13.7        | 288    | 16 | O66454 | O66454 aquifex aeo  |
| 15         | 392    | 13.7        | 289    | 17 | Q97XZ7 | Q97xz7 sulfolobus   |
| 16         | 384    | 13.4        | 334    | 10 | Q9S2E1 | Q9szel arabidopsis  |

90 285 9.9 305 16 Q98N82 rhizobium 1  
 91 284 9.9 303 16 Q8XU8 ralstonia s  
 92 282.5 9.9 329 13 Q7SXU4 Q7xj4 brachydanio  
 93 281.5 9.8 298 16 Q8X8D4 Q8x8d4 escherichia  
 94 280 9.8 295 16 Q92PN5 Q92pn5 rhizobium m  
 95 279.5 9.8 292 16 Q8Z8Q9 Q8z8q9 salmonella  
 96 279.5 9.8 345 5 Q86R98 Q86r98 drosophila  
 97 279 9.7 298 16 Q92T07 Q92tg7 rhizobium m  
 98 278 9.7 313 16 Q8U8K6 Q8u8k6 agrobacteri  
 99 277.5 9.7 359 16 Q8FBG0 Q8fbg0 escherichia  
 100 277 9.7 285 16 Q7U3K2 Q7u3k2 synechococc

## ALIGNMENTS

RESULT 1  
 Q98XK2 PRELIMINARY; PRT; 547 AA.  
 ID Q98XK2  
 AC Q98XK2; 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Cytokine-like nuclear factor n-pac.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA New L., Han J.;  
 RT "A novel cytokine-like nuclear factor, n-pac";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF326966; AAK1524.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:003677; F:DNA binding; IEA.  
 DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.  
 DR GO; GO:0006098; P:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR006115; 6PGD NAD.  
 DR InterPro; IPR00637; AT hook.  
 DR InterPro; IPR00313; PWMP domain.  
 DR Pfam; PF02178; AT hook; 1.  
 DR Pfam; PF03446; NAD binding\_2; 1.  
 DR Pfam; PF00855; PWMP; 1.  
 DR SMART; SM00384; AT hook; 1.  
 DR PROSITE; PS50812; PWMP; 1.  
 DR SEQUENCE 547 AA; 59827 MW; C7D785CCBF83204A CRC64;

Query Match 98.1%; Score 2811; DB 4; Length 547;  
 Best Local Similarity 98.7%; Pred. No. 4.9e-189;  
 Matches 546; Conservative 0; Mismatches 1; Indels 6; Gaps 1;  
 QY 1 MAAVSLRLGDLVWGKLGRYPPWPKIVNPKDLKKPRGKCFVFKFGTGHAWIKVEQL 60  
 DB 1 MAAVSLRLGDLVWGKLGRYPPWPKIVNPKDLKKPRGKCFVFKFGTGHAWIKVEQL 60  
 QY 61 KPYHAKEEMIKNGKRFQAVDAVEEFLRRAKGDQTS SHNSDDKNRNSSEERSRP 120  
 DB 61 KPYHAKEEMIKNGKRFQAVDAVEEFLRRAKGDQTS SHNSDDKNRNSSEERSRP 120  
 QY 121 NSGDEKRLSLSEGKVKNNMGEKKRVSSGSSERGSPLKRAEQSPKRGPRPKDEK 180  
 DB 121 NSGDEKRLSLSEGKVKNNMGEKKRVSSGSSERGSPLKRAEQSPKRGPRPKDEK 180  
 QY 181 LTIPESSTVKGMAAGPMAAFKMQPTASEPVKDADPHFHHLLSOTKPAVCYQAITKKLK 240  
 DB 181 LTIPESSTVKGMAAGPMAAFKMQPTASEPVKDADPHFHHLLSOTKPAVCYQAITKKLK 240  
 QY 241 ICEETGTSIQADSTAVNGSIPTDKKIGFLGLMGSGIVSNLLKMGHTVTWNRTA 300  
 DB 241 ICEETGTSIQADSTAVNGSIPTDKKIGFLGLMGSGIVSNLLKMGHTVTWNRTA 300

QY 301 EKCDLFIQEGARLGRTPAEVSTCITITFACVSDPKAAKDLVLGPSGLVQGIKPGKCYDM 360  
 DB 301 EK-----EGARLGRTPAEVSTCITITFACVSDPKAAKDLVLGPSGLVQGIKPGKCYDM 354  
 QY 361 STVDADTVTELAQVTVSRGGFLEAPVSGNOOLSDNGMLVILAAAGDRLGYEDCSCFOAM 420  
 DB 361 STVDADTVTELAQVTVSRGGFLEAPVSGNOOLSDNGMLVILAAAGDRLGYEDCSCFOAM 414  
 QY 421 GKTSPFLGVEGNAAKMMLIVNMVQGSFMATTAEGTLTAHVTCGSOQTLLDILNQGLASI 480  
 DB 421 GKTSPFLGVEGNAAKMMLIVNMVQGSFMATTAEGTLTAHVTCGSOQTLLDILNQGLASI 474  
 QY 481 FLQKQCNILQGNFKPFDLYIKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKDOS 540  
 DB 475 FLQKQCNILQGNFKPFDLYIKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKDOS 534  
 QY 541 DNDMSAVRAYIH 553  
 DB 535 DNDMSAVRAYIH 547

## RESULT 2

Q922P9 PRELIMINARY; PRT; 546 AA.  
 ID Q922P9  
 AC Q922P9;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE RIKEN cDNA 3930401K13 gene.  
 GN NPAC OR 3930401K13RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006893; AAH06893.1; -;  
 DR MGD; MGI:1921272; Npac.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.  
 DR GO; GO:0006098; P:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR006115; 6PGD NAD.  
 DR InterPro; IPR00637; AT hook.  
 DR InterPro; IPR00313; PWMP domain.  
 DR Pfam; PF02178; AT hook; 1.  
 DR Pfam; PF03446; NAD binding\_2; 1.  
 DR Pfam; PF00855; PWMP; 1.  
 DR SMART; SM00384; AT hook; 1.  
 DR PROSITE; PS50812; PWMP; 1.  
 DR SEQUENCE 546 AA; 59715 MW; F5D2090DE1F64723 CRC64;

Query Match 96.6%; Score 2767.5; DB 11; Length 546;  
 Best Local Similarity 97.3%; Pred. No. 5.6e-186;  
 Matches 538; Conservative 5; Mismatches 3; Indels 7; Gaps 2;  
 QY 1 MAAVSLRLGDLVWGKLGRYPPWPKIVNPKDLKKPRGKCFVFKFGTGHAWIKVEQL 60  
 DB 1 MAAVSLRLGDLVWGKLGRYPPWPKIVNPKDLKKPRGKCFVFKFGTGHAWIKVEQL 60  
 QY 61 KPYHAKEEMIKNGKRFQAVDAVEEFLRRAKGDQTS SHNSDDKNRNSSEERSRP 120  
 DB 61 KPYHAKEEMIKNGKRFQAVDAVEEFLRRAKGDQTS SHNSDDKNRNSSEERSRP 120  
 QY 121 NSGDEKRLSLSEGKVKNNMGEKKRVSSGSSERGSPLKRAEQSPKRGPRPKDEK 180  
 DB 121 NSGDEKRLSLSEGKVKNNMGEKKRVTSADRSKC-LKRAEQSPKRGPRPKDEK 179  
 QY 181 LTIPESSTVKGMAAGPMAAFKMQPTASEPVKDADPHFHHLLSOTKPAVCYQAITKKLK 240



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Db 180 LTIPESSTVKGMMAGPMAAFKWPQTATEPVKADDPHFHFLLSQTEKPAVCYQAITKKLK 239
QY 241 ICEETGTSIOAADSTAVNGSIITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVWNR 300
Db 240 ICEETGTSIOAADSTAVNGSIITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVWNR 299
QY 301 EKCDLFIQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGIRPGKCYVDM 360
Db 300 EK-----EGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGIRPGKCYVDM 353
QY 361 STVDADTVELAQVIVSRGGRLEAPVSGNQLSNDGMLVILAAAGDGLYEDCSCFOAM 420
Db 354 STVDADTVELAQVIVSRGGRLEAPVSGNQLSNDGMLVILAAAGDGLYEDCSCFOAM 413
QY 421 GTSFFLGEVGNAAKMWMLIVNMVQGSFMATIAEGLTLAHTVTSQOQLDILNOGQLASI 480
Db 414 GTSFFLGEVGNAAKMWMLIVNMVQGSFMATIAEGLTLAHTVTSQOQLDILNOGQLASI 473
QY 481 FLDQKQCNILQGNFKPDPFYLYIKQDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS 540
Db 474 FLDQKQCNILQGNFKPDPFYLYIKQDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS 533
QY 541 DNDSAVYRAYIH 553
Db 534 DNDSAVYRAYIH 546

RESULT 3
Q9CYQ1 PRELIMINARY; PRT; 546 AA.
AC Q9CYQ1,
DC Q9CYQ1,
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3930401K13RIK protein.
GN NPAC OR 3930401K13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryo;
EX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK014456; BAB29363.1; -.
DR MGD: MGI:1921272; Npac.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR GO: 0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO: 0006098; P:pentose-phosphate shunt; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR006115; 6PGD_NAD.
DR DrPro: IPR000637; AT_hook.

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DR InterPro: IPR000313; PWWP domain.
DR Pfam: PF02178; AT_hook; 1.
DR Pfam: PF03446; NAD_binding_2; 1.
DR Pfam: PF00855; PWWP; 1.
DR SMART: SM00384; AT_hook; 1.
DR PROSITE: PS00812; PWWP; 1.
SQ SEQUENCE 546 AA; 59744 MW; B3AC1562477ABC1F CRC64;

Query Match 95.8%; Score 2745.5; DB 11; Length 546;
Best Local Similarity 96.6%; Pred. No. 2e-184;
Matches 534; Conservative 8; Mismatches 4; Indels 7; Gaps 2;

QY 1 MAAVSLRLGDLVWVKLGIRYPPWPGKI VNPDKLKKPRGKKCFVVFEGTDEHAWIKVEQL 60
Db 1 MAAVSLRLGDLVWVKLGIRYPPWPGKI VNPDKLKKPRGKKCFVVFEGTDEHAWIKVEQL 60
QY 61 KPYHAHKEEMIKKNGKRFQQA VDAVEEFLRAKGDQTSSTNSDDKNNRNSSEERSRP 120
Db 61 KPYHAHKEEMIKKNGKRFQQA VDAVEEFLRAKGDQTSSTNSDDKNNRNSSEERSRP 120
QY 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKFLKRAQOSPRKGRPPKDEKD 180
Db 121 NSGDEKRLSLSEGKVKKNMGEGKKRVSSGSSERGSKFLKRAQOSPRKGRPPKDEKD 179
QY 181 LTIPESSTVKGMMAGPMAAFKWPQTATEPVKADDPHFHFLLSQTEKPAVCYQAITKKLK 240
Db 180 LTIPESSTVKGMMAGPMAAFKWPQTATEPVKADDPHFHFLLSQTEKPAVCYQAITKKLK 239
QY 241 ICEETGTSIOAADSTAVNGSIITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVWNR 300
Db 240 ICEETGTSIOAADSTAVNGSIITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVWNR 299
QY 301 EKCDLFIQEGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGIRPGKCYVDM 360
Db 300 EK-----EGARLGRTPAEVSTCDITFACVSDPKAAKDLVLGPGSVLGIRPGKCYVDM 353
QY 361 STVDADTVELAQVIVSRGGRLEAPVSGNQLSNDGMLVILAAAGDGLYEDCSCFOAM 420
Db 354 STVDADTVELAQVIVSRGGRLEAPVSGNQLSNDGMLVILAAAGDGLYEDCSCFOAM 413
QY 421 GTSFFLGEVGNAAKMWMLIVNMVQGSFMATIAEGLTLAHTVTSQOQLDILNOGQLASI 480
Db 414 GTSFFLGEVGNAAKMWMLIVNMVQGSFMATIAEGLTLAHTVTSQOQLDILNOGQLASI 473
QY 481 FLDQKQCNILQGNFKPDPFYLYIKQDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS 540
Db 474 FLDQKQCNILQGNFKPDPFYLYIKQDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS 533
QY 541 DNDSAVYRAYIH 553
Db 534 DNDSAVYRAYIH 546

RESULT 4
Q9BT11 PRELIMINARY; PRT; 523 AA.
AC Q9BT11,
DC Q9BT11,
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN cDNA 3930401K13 gene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003693; AAH03693.1; -.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.

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DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.  
 DR GO; GO:0006099; P:pentose-phosphate shunt; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR006115; 6PGD\_NAD.  
 DR InterPro; IPR000637; AT hook.  
 DR InterPro; IPR000313; PWP domain.  
 DR Pfam; PF02178; AT hook; 1.  
 DR Pfam; PF03446; NAD\_binding\_2; 1.  
 DR Pfam; PF00855; PWP; 1.  
 DR SMART; SM00384; AT hook; 1.  
 DR PROSITE; PS00812; PWP; 1.  
 FT NON\_TER.  
 SQ SEQUENCE 523 AA; 57215 MW; ED3E2853938A211F CRC64;  
 Query Match 93.6%; Score 2693.5; DB 4; Length 523;  
 Best Local Similarity 96.7%; Pred. No. 4.2e-180;  
 Matches 522; Conservative 0; Mismatches 1; Indels 17; Gaps 1;  
 QY 14 GKLGRYPWPVGKIVNPPDKLPRGKKCFVFFGTEHDHAWIKVEOLKPYHAKEEMIKI 73  
 Db 1 GKLGRYPWPVGKIVNPPDKLPRGKKCFVFFGTEHDHAWIKVEOLKPYHAKEEMIKI 60  
 QY 74 NKGKRFQQAADVAEEFLRAKGDQTSNHSDDKNRNSSEERSPNSGDEKRLSLSE 133  
 Db 61 NKGKRFQQAADVAEEFLRAKGDQTSNHSDDKNRNSSEERSPNSGDEKRLSLSE 120  
 QY 134 GKVKQMGKGRVSSGSSGSKSLKRAQSGSKRGRPPKDEKDLTIPSSVTYKGMW 193  
 Db 121 GKVKQMGKGRVSSGSSGSKSLKRAQSGSKRGRPPKDEKDLTIPSSVTYKGMW 180  
 QY 194 AGPMAFKQPTASEPVKDADPHFHLFSQTEKPAVCQAATKIKICEETGTSIOA 253  
 Db 181 AGPMAFKQPTASEPVKDADPHFHLFSQTEK-----ETGTSIOA 223  
 QY 254 ADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQSGARL 313  
 Db 224 ADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFIQSGARL 283  
 QY 314 GRTPAEVSCTDITFACVSDPKAAKDLVLPSPVLOGIRPKCYVDMSTVDADTVTELAQ 373  
 Db 284 GRTPAEVSCTDITFACVSDPKAAKDLVLPSPVLOGIRPKCYVDMSTVDADTVTELAQ 343  
 QY 374 VIVSRGGRFLEAPVSGNQQLSDNGLVLAAGDRGLYEDCSCFQAMGKTSFPLGSGVNA 433  
 Db 344 VIVSRGGRFLEAPVSGNQQLSDNGLVLAAGDRGLYEDCSCFQAMGKTSFPLGSGVNA 403  
 QY 434 AKMMLIVNVVQGSFMATIAEGLTLAHTVGTQSQTLLDILNQGLASIFLDKQCNILQGN 493  
 Db 404 AKMMLIVNVVQGSFMATIAEGLTLAHTVGTQSQTLLDILNQGLASIFLDKQCNILQGN 463  
 QY 494 FKPDFYLYKIQDLRLAIALGDVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYRAYTH 553  
 Db 464 FKPDFYLYKIQDLRLAIALGDVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYRAYTH 523  
 RESULT 5  
 Q8T079 PRELIMINARY; PRT; 602 AA.  
 AC Q8T079; Q9VL51;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LD22344p (CG4747-PA).  
 GN BEST:LD22483 OR BEST:LD29743 OR CG4747.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Blanton R.C., Rogers Y.H., Blazey Y.H., Blazey C.R., Gabor G.L., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D., Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Botchan M.R., Bouck J.P., Brokstein P., Brotier P., Borkova D., Botsam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Hernandez J.R., Houck J., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei G., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner C., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 "The genome sequence of Drosophila melanogaster";  
 Science 287:2185-2195(2000).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradycky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 "Annotation of Drosophila melanogaster genome";  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RN SEQUENCE FROM N.A.  
 RP FlyBase;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY069497; AAL39842.1; -  
 DR EMBL; AE003627; AAF52846.3; -  
 DR FlyBase; FBgn0043456; BEST:LD22483.  
 DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.  
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.  
 DR InterPro; IPR006115; 6PGD\_NAD.  
 DR InterPro; IPR000313; PWP domain.

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DR Pfam; PF03446; NAD_binding_2; 1.
DR Pfam; PF00855; PWWP; 1.
DR SMART; SM00293; PWWP; 1.
DR PROSITE; PS00812; PWWP; 1.
SQ SEQUENCE 602 AA; 65252 MW; E004EEC610C32625 CRC64;

Query Match 27.8%; Score 796.5; DB 5; Length 602;
Best Local Similarity 32.8%; Pred. No. 1.8e-47;
Matches 192; Conservative 110; Mismatches 225; Indels 59; Gaps 13;

QY 10 DLVWGLKGRYPWPGKIVNPKDL---KKPRGKCKFFVKFEGTEDHAMKVEQKLPYHA- 65
Db 24 DLIWAKMGFTWPGMIVDPDLDSQQRRANTKCVF--PFGSRNFAWIEENIKPFEPG 81
QY 66 HKEWMKINKKRRFQQAQVDAVEEFLRRAKGKDQTSNHSDDKNNRNSSEERSPNSGDE 125
Db 82 WKEELAKVSKPAAFRHMTDIEKYIDDAEVEQVNSCGAPNHATEADFKIR--DGLD 139
QY 126 KRKLSLSEGVKYNMGEGKKRVSSGSSRG-----SKSPL-----KRAQRQS 167
Db 140 SEEIVGEEATAGNNGVVAHV--GSPDEGDGLDVEINADSSASPVTSPAVTTKAAGKRT 197
QY 168 PR-----KRGPRPKDEKDLITPESSTVKGMAAGPMAAFKQWPTAS-BPVKQADP 215
Db 198 PKAKSVAAATSVKSGSAKSAQKRTSAQOSP-----SGPSNAKRGKRDVSGEALQDADE 252
QY 216 -----HFHFLLSQTEKPAVCYQALTKKLKICEETGTSIQAADSTAVNGSIT 264
Db 253 ASSTPTGRRRRETALLASIAAKAPNAIALDRPVTRPQAVIDMSRSNTLIADRIDV 312
QY 265 PTDKKIGFLGLGMSGIVSNLLKMGHTVTVWNRPAEKCDLFIQEGARLGRTPAEVSTC 324
Db 313 PSEQTGFLGLGMSGIVSNLLKMGHTVTVWNRPAEKCDLFIQEGARLGRTPAEVSTC 372
QY 325 DITFACVSDPKAAKDLVLPSPGVQIGRP--GKCYVDMSTVDATVTELAQVIVSRGRGF 382
Db 373 DVIFCCVSDPKAAKDLVLPSPGVQIGRP--GKCYVDMSTVDATVTELAQVIVSRGRGF 431
QY 383 LEAPVSGNQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLVNM 442
Db 432 LEAQHSRQEAAGMILLIAGDRSFECHSCFKTAKNTFFLGNIGNACKNLLIQT 491
QY 443 VQGSFMATIAEGLTIAHVTGOSQOITLLDILNQGLASIFLDQKQNILOGNFKPDFYLKY 502
Db 492 ILGVSILVGLAEALADRFSLINDIIDIFDLTSMKSPMLLAKGKAKGDFNFQQPLSH 551
QY 503 IQKDLRLAIALGDVAVNHTPMAAAANEVYKRAKALDOSDNDMSAVY 548
Db 552 MQRDRLVLNNAENLDQSMFVTSITNEVFKTRKLGYSSEHDSAVF 597
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RESULT 6
Q84VC8 PRELIMINARY; PRT; 293 AA.
AC Q84VC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical protein).
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C.,
RA Goff S., Glazebrook J.,
RT "Identification of Rice (Oryza sativa) Proteins Linked to the Cyclin-
RT Mediated Regulation of the Cell Cycle."
RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
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[2]
RN SEQUENCE FROM N.A.
RP TISSUE-Panicle;
RC Moriguchi K., Ito Y., Yamazaki Y., Kurata N.;
RA "Finding of various plant nuclear proteins using yeast nuclear
RT transportation trap system - a proteomal approach."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY224558; AA072678.1; --
DR EMBL; AB110167; BAC78559.1; --
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxylase); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxoisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
KW Hypothetical protein.
SQ SEQUENCE 293 AA; 30496 MW; 2362B7AC4EE52038 CRC64;

Query Match 25.4%; Score 727; DB 10; Length 293;
Best Local Similarity 52.1%; Pred. No. 5e-43;
Matches 146; Conservative 49; Mismatches 85; Indels 0; Gaps 0;

QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVWNRPAEKCDLFIQEGARLGRTPAEVSTCITP 328
Db 2 EVGFLGIGMGKAAANLLRHGFRVTVMNRTLSKCQELVALGAAGVETPAAVAKCRYTI 61
QY 329 ACVSDPKAAKDLVLPSPGVQIGRP--GKCYVDMSTVDATVTELAQVIVSRGRFLEAPVS 388
Db 62 AMLSDPSAALSVDPDKGVLEQIGEGKGYVDMSTVDAATSKISEAIKQKGAFAEAPVS 121
QY 389 GNQOLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLVNMVQGSFM 448
Db 122 GSKPAEDGQQLVILAAGDKVLYDDMPAFDVLGKKSFFLGEVGNAAKMLVNMVQGSFM 181
QY 449 ATTAEGTLIAHVTGOSQOITLLDILNQGLASIFLDQKQNILOGNFKPDFYLKYIKDLR 508
Db 182 NALSEGSLADNSGLSPQTLTLLDVLDAIANPFLKGPMSLQGSYNPAFPFLKHQKQDMR 241
QY 509 LAIALGDVAVNHTPMAAAANEVYKRAKALDOSDNDMSAVY 548
Db 242 LALALGDENAVSMPTVAASNEAFKARSGLGLDLDFAVY 281

RESULT 7
Q94B07 PRELIMINARY; PRT; 289 AA.
AC Q94B07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gamma hydroxybutyrate dehydrogenase (EC 1.1.1.61).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Breithreuz K.E., Van Cauwenberghe O.R., Allen W.L., Jakobs C.,
RA Talibi D., McLean M.D., Andre B., Shelp B.J.;
RA "Plant gamma-hydroxybutyrate dehydrogenase, a novel fermentation
RT enzyme."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY041183; AAK94781.1; --
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxylase); IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
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DR InterPro: IPR002204; 3hydroxisobut_dh.
DR InterPro: IPR006183; 6PGD_NAD.
DR InterPro: IPR006115; 6PGD_NAD.
DR Pfam: PF03446; NAD binding 2; 1.
DR PRINTS: PR00076; 6PGDHDRGNASE.
DR PROSITE: PS00895; 3_HYDROXYISOBUT_DH; 1.
KW Oxidoreductase.
SQ SEQUENCE 289 AA; 30678 MW; 3E6715DFF96593D6 CRC64;

Query Match 24.3%; Score 697; DB 10; Length 289;
Best Local Similarity 49.6%; Pred. No. 6.2e-41;
Matches 140; Conservative 49; Mismatches 93; Indels 0; Gaps 0;

QY 269 KIGFLGLGMSGIGVSNLLKMGHTVTVNNTAEKCDLFIQEGARLGRTPAEVSVTCDITF 328
DB 2 EVGFLGLGMSGIGVSNLLKMGHTVTVNNTAEKCDLFIQEGARLGRTPAEVSVTCDITF 61

QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTETLAQVIVSRGGRFLEAPVS 388
DB 62 AMLSDPCAALSVVFDKGVLEQICGKGYIDMSTVDAETSLKINEAITGKGRFVEGPVS 121

QY 389 GNOQLNSDGMVLILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIIVNMVQGSFM 448
DB 122 GSKKPAEDQGLIILAAGDKALFEESIPAFDVLGKESFYLGVGVNGAKMKLIIVNMVQGSFM 181

QY 449 ATIAEGLTLAHVTGOSQOTLLDILNOGQLASIFLDQKCONILQGNFKPDPFLYKIQOKLR 508
DB 182 NAFSEGLVLADKSGLSSTLLDILGAMTNMFKGKGSFNMKSSYPFAPFLKHQOKDWR 241

QY 509 LAIALGDVANHPTPMAAANAENVYKRAKALDQSDNDMSAVYRA 550
DB 242 LALALGDENAVSMPVAAAANAENAFKXRSGLGLDLSFVIEA 283

RESULT 8
Q9LSV0 PRELIMINARY; PRT; 289 AA.
AC Q9LSV0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2003 (TrEMBLrel. 15, Last sequence update)
DE Dehydrogenase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Nakamura Y.;
RA MEDLINE=20277480; PubMed=10819329;
RP SEQUENCE FROM N.A.
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty F1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
DR EMBL; AB025639; BAB01322.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro: IPR002204; 3hydroxisobut_dh.
DR InterPro: IPR006183; 6PGD.
DR InterPro: IPR006115; 6PGD_NAD.
DR Pfam: PF03446; NAD binding 2; 1.
DR PRINTS: PR00076; 6PGDHDRGNASE.
DR PROSITE: PS00895; 3_HYDROXYISOBUT_DH; 1.
SQ SEQUENCE 289 AA; 30691 MW; 3E67002A19706636 CRC64;

Query Match 24.2%; Score 695; DB 10; Length 289;
Best Local Similarity 49.6%; Pred. No. 8.6e-41;
Matches 140; Conservative 49; Mismatches 93; Indels 0; Gaps 0;

QY 269 KIGFLGLGMSGIGVSNLLKMGHTVTVNNTAEKCDLFIQEGARLGRTPAEVSVTCDITF 328
DB 2 EVGFLGLGMSGIGVSNLLKMGHTVTVNNTAEKCDLFIQEGARLGRTPAEVSVTCDITF 61

QY 329 ACVSDPKAAKDLVLGSPGVLOGIRPKCYVDMSTVDADTVTETLAQVIVSRGGRFLEAPVS 388
DB 62 AMLSDPCAALSVVFDKGVLEQICGKGYIDMSTVDAETSLKINEAITGKGRFVEGPVS 121

QY 389 GNOQLNSDGMVLILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMWLIIVNMVQGSFM 448
DB 122 GSKKPAEDQGLIILAAGDKALFEESIPAFDVLGKESFYLGVGVNGAKMKLIIVNMVQGSFM 181

QY 449 ATIAEGLTLAHVTGOSQOTLLDILNOGQLASIFLDQKCONILQGNFKPDPFLYKIQOKLR 508
DB 182 NAFSEGLVLADKSGLSSTLLDILGAMTNMFKGKGSFNMKSSYPFAPFLKHQOKDWR 241

QY 509 LAIALGDVANHPTPMAAANAENVYKRAKALDQSDNDMSAVYRA 550
DB 242 LALALGDENAVSMPVAAAANAENAFKXRSGLGLDLSFVIEA 283

RESULT 9
Q8RWFL PRELIMINARY; PRT; 343 AA.
AC Q8RWFL;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Atlg17650).
GN Atlg17650.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; genome
RA "Full-length messenger RNA sequences greatly improve genome
RA annotation."
RN Genom. Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA "Full-length cDNA from Arabidopsis thaliana."
RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA "Arabidopsis ORF clones."
RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093135; AA013134.1; -.

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DR EMBL; AY049298; AAK63640.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SQ SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;

Query Match 19.6%; Score 562; DB 10; Length 248;
Best Local Similarity 51.7%; Pred. No. 1.5e-31;
Matches 109; Conservative 36; Mismatches 66; Indels 0; Gaps 0;

QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
DB 2 EVGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
QY 329 ACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDMSTVDADTVTVELAQVIVSRGRFLEAPVS 388
DB 62 AMLSDPCAALSVVDFKGVLEQICGKGYIDMSTVDAETSLKINEAITGKGRFVEGPPVS 121
QY 389 GNOQLSNDGMLVTLAAGDRGLYEDCSSCFQAMGKTSFELGEGVNAKMLVNMVQGSFM 448
DB 122 GSKKPAEDGQLIILAAGDKALFEESIPAFDVLGKRSFYLGQVNGAKMKLIVNMVQGSFM 181
QY 449 ARTAEGLTIAHVTGSGSQOQLLILNQGLAS 479
DB 182 NAFSEGLVLADKSLSSDFTLLDLDLGAMTN 212

RESULT 12
Q8LQJ7 PRELIMINARY; PRT; 343 AA.
AC Q8LQJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 22, Last sequence update)
DE Putative gamma hydroxybutyrate dehydrogenase.
GN B1151A10.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:B1151A10."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003413; BAB91904.1; -.
DR Gramene; Q8LQJ7; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SQ SEQUENCE 343 AA; 35481 MW; 195ABBEA048F84D CRC64;

Query Match 19.5%; Score 560; DB 10; Length 343;
Best Local Similarity 40.5%; Pred. No. 3.3e-31;
Matches 125; Conservative 49; Mismatches 83; Indels 52; Gaps 4;

QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
DB 2 EVGFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTCDITF 328
QY 329 ACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDMSTVDADTVTVELAQVIVSRGRFLEAPVS 388
DB 62 AMLSDPCAALSVVDFKGVLEQICGKGYIDMSTVDAETSLKINEAITGKGRFVEGPPVS 121
QY 389 GNOQLSNDGMLVTLAAGDRGLYEDCSSCFQAMGKTSFELGEGVNAKMLVNMVQGSFM 448
DB 122 GSKKPAEDGQLIILAAGDKALFEESIPAFDVLGKRSFYLGQVNGAKMKLIVNMVQGSFM 181
QY 449 ARTAEGLTIAHVTGSGSQOQLLILNQGLAS 479
DB 182 NAFSEGLVLADKSLSSDFTLLDLDLGAMTN 212

RESULT 13
Q8TT25 PRELIMINARY; PRT; 300 AA.
AC Q8TT25;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
DE 3-hydroxyisobutyrate dehydrogenase.
GN MA0614.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE-21929760; PubMed-11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Anoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McSwan P., McKernan K., Tallamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hederich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010722; AAM04058.1; -.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
KW Complete proteome.
SQ SEQUENCE 300 AA; 32287 MW; FB1E7A8A8A8A7E CRC64;

Query Match 13.9%; Score 397; DB 17; Length 300;
Best Local Similarity 31.8%; Pred. No. 7.8e-20;
Matches 90; Conservative 47; Mismatches 144; Indels 2; Gaps 1;

QY 267 DKXI--GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTC 324
DB 7 DKNITGVIGLGMGSFASNLSSRGYNVHVYNTKEKAQPLIERGATPHSTPRELASVA 66
QY 325 DITFACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDMSTVDADTVTVELAQVIVSRGRFLE 384

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DB 52 KVGFGLGIMPASNLINAGCDVTVVNRTRSKCDPLLSLCAKYEPSPADVASSCDVTF 111
QY 329 ACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDMSTVDADTVTVELAQVIVSRGRFLEAPVS 388
DB 112 AMLADPESAVEVACGANGAAGMAPGKGYVDVSTVDAATSKLGHITSTGASFLERC-- 169
QY 389 GNOQLSNDGMLVTLAAGDRGLYEDCSSCFQAMGKTSFELGEGVNAKMLVNMVQGSFM 424
DB 170 -----DFSSCTVGPMLTRYLFSRLQFQAQKSSQKMGCSFLP 206
QY 425 ---PFLGEGVNAKMLVNMVQGSFMATIAEGLTIAHVTGSGSQOQLLILNQGLASIF 481
DB 207 QSRFFLGVDGKADMKLVNMVQGSFMVFSFSEGLLSLSEKVGLDPTNLVEVTSQGISAPM 266
QY 482 LDQKQCNILQGNFKDEVLKYIQDLRLAIALGDVNNHPTMAAANEVYKAKALDQSD 541
DB 267 FSLGPGSMVKAAIPTAFPLKHOQDLRLALALAESVSQSIPTVAANELYKVAKSLGLAD 326
QY 542 NDMSAVYRA 550
DB 327 QDFSAVIEA 335

RESULT 13
Q8TT25 PRELIMINARY; PRT; 300 AA.
AC Q8TT25;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
DE 3-hydroxyisobutyrate dehydrogenase.
GN MA0614.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE-21929760; PubMed-11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Anoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McSwan P., McKernan K., Tallamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hederich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010722; AAM04058.1; -.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHDRGNASE.
KW Complete proteome.
SQ SEQUENCE 300 AA; 32287 MW; FB1E7A8A8A8A7E CRC64;

Query Match 13.9%; Score 397; DB 17; Length 300;
Best Local Similarity 31.8%; Pred. No. 7.8e-20;
Matches 90; Conservative 47; Mismatches 144; Indels 2; Gaps 1;

QY 267 DKXI--GFLGLGMSGIVSNLLKMGHTVTVMNRTAEKCDLFTQEGARLGRTPAEVSTC 324
DB 7 DKNITGVIGLGMGSFASNLSSRGYNVHVYNTKEKAQPLIERGATPHSTPRELASVA 66
QY 325 DITFACVSDPKAAKDLVLGPGSVLGQIRPGKCYVDMSTVDADTVTVELAQVIVSRGRFLE 384

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Db 67 DIIMTSLTDEAAVNSVAFGEDGLNGAKKGLWIDLSTIDPSSSVKHAABAAKAGLERLD 126
QY 385 APVSGNQQLSNDGMLVILAAAGRGLYEDSCSCFQAMGKTSFFELGEGVNAAKMMLVNMVQ 444
Db 127 TPVVGSKLASKEGELIILVGGQEVLRKEHFKNLGKRSVILGADGNGHKMLALNHL 186
QY 445 GSFMATIAGLTLAHTVGTGSOOTLLDILNQGLASIFLDQKQNILOQGNFKPDFYLYIQ 504
Db 187 GLLAESFSEALVFSQKLGDAKTFVETINNTPIRVISQKGRIVEGNEFPAFSLNLA 246
QY 505 KDLRLAIALGDVNHPTPMAAANEVYKRAKALDQSDNDMSAV 547
Db 247 KDLRLVNEQITKTGAILPMTKVSIIEYSRTVQNGEGQKDFSVI 289

RESULT 14
O66454 PRELIMINARY; PRT; 288 AA.
AC O66454;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-OCT-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 3-hydroxyisobutyrate dehydrogenase.
GN HIBD OR AQ_038.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000670; AAC06408.1; -.
DR PIR; C70303; C70303.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxylase); IEA.
DR GO; GO:0006038; P:pentose-phosphate shunt; IEA.
DR InterPro; IPR008927; 6GDH_C_like.
DR InterPro; IPR006183; 6PGD.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR Complete proteome.
KW SEQUENCE 288 AA; 31788 MW; 60E79AF4954D4294 CRC64;

Query Match 13.7%; Score 392.5; DB 16; Length 288;
Best Local Similarity 31.7%; Pred. No. 1.5e-19;
Matches 90; Conservative 61; Mismatches 132; Indels 1; Gaps 1;

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDIT 327
Db 2 KVGFIGLGLRAIAKELIEQGVLELVNRTLSKAHEFAKETGAETVSSPADLINKVDV 61
QY 328 FACVSDPKAAKDLVLGSGVLQGRPGKCYVDMSTVDADTVTELAQVIVSRGGRLEAPV 387
Db 62 FVIVFDSQAESEVIFGKGLVKGDIGKGTVDMTNHYLAQKAYEELKGLGAFYLDAPV 121
QY 388 SGNQQLSNDGMLVILAAAGRGLYEDSCSCFOAMGKTSFFELGEGVNAAKMMLVNMVQSGF 447
Db 122 LGSVIPALKGELTIVGDKKEFENKPLFEKFCRAIYILGEAGMGKMLVNMVILGGI 181
QY 448 MATIAGLTLAHTVGTGSOOTLLDILNQGLASIFLDQKQNILOQGNFKPDFYLYIQKOL 507
Db 182 MEVLAIAIAGERAGIDKETLINVLDNGAGKSYILDVKKKLEEDSFTHFSVNLIIKDL 241
QY 508 RLALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVRAY 551
Db 242 HYAQDLIKDLGLFSFTTAAVVKETYGLARKGFGNLDPSAVYKLF 285

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RESULT 15
Q97XZ7 PRELIMINARY; PRT; 289 AA.
ID Q97XZ7;
AC Q97XZ7;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Oxidoreductase.
GN SSO1560.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OX Sulfolobus
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Etrauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006770; AAK41774.1; -.
DR PIR; G90314; G90314.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxylase); IEA.
DR GO; GO:0006038; P:pentose-phosphate shunt; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxibsubut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF03446; NAD binding 2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
DR PROSITE; PS00030; REM_RNP_1; 1.
KW Complete proteome.
SQ SEQUENCE 289 AA; 31025 MW; 4EEA33390300E7C7 CRC64;

Query Match 13.7%; Score 392; DB 17; Length 289;
Best Local Similarity 29.3%; Pred. No. 1.7e-19;
Matches 83; Conservative 68; Mismatches 132; Indels 0; Gaps 0;

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGRTPAEVSTCDITF 328
Db 2 KVGFIGLGLMGFPFNASLLKAGYDLTVNRTIEKAEKLGKMGAKVAHSPREVAEVSIEVI 61
QY 329 ACVSDPKAAKDLVLGSGVLQGRPGKCYVDMSTVDADTVTELAQVIVSRGGRLEAPVS 388
Db 62 SMVTDAPDVEVIFGEGVVKSNKGLIFVDMSTNSPEFAKKVTKRLSEYGEFLDAPV 121
QY 389 SGNQQLSNDGMLVILAAAGRGLYEDSCSCFOAMGKTSFFELGEGVNAAKMMLVNMVQSGFM 448
Db 122 GGDGKAREGLTITMVGKEDVFKRVEPIFKAMGKNIHVGDVSGQALKLCNQVVVALNM 181
QY 449 ATTAEGTLTAHTVGTGSOOTLLDILNQGLASIFLDQKQNILOQGNFKPDFYLYIQKDLR 508
Db 182 VSVVEGILLARSIGIDDDKLFVSLVSTGAANSFTVQYVLPKIMKGLNPGFKAHLKXDLK 241
QY 509 LALALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVRAY 551
Db 242 YAMEIANSKSLPLGLTSLALQLYNAMVSLGIGELGTQGLVKVY 284

RESULT 16
Q9SZE1

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Q9SZE1 PRELIMINARY; PRT; 334 AA.

AC Q9SZE1

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein (Putative dehydrogenase).

GN F1915.150 OR AT4G29120.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,

RA Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Arabidopsis sequencing project;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,

RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,

RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseima E.,

RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,

RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,

RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RT "Full length cDNA of gene AT4g29120 (GI:7269810).";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M.,

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.;

RT "Full length cDNA of gene AT4g29120 (GI:7269810).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RA EMBL; AL078470; CAB43926.1; -

DR EMBL; AL161574; CAB79670.1; -

DR EMBL; AF370197; AAK4012.1; -

DR EMBL; AY062952; AAL33784.1; -

DR PIR; T08967; T08967.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. . .); IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.

DR InterPro; IPR006183; 6PGD.

DR InterPro; IPR006115; 6PGD NAD.

DR InterPro; IPR002227; Tyrosinase.

DR Pfam; PF03446; NAD binding 2; 1.

DR PRINTS; PR00076; 6FGDHRGNASE.

DR PROSITE; PS00498; TYROSINASE\_2; 1.

KW Hypothetical protein.

SQ SEQUENCE 334 AA; 35371 MW; EC0038096DB836BA CRC64;

Query Match 13.4%; Score 384; DB 10; Length 334;

Best Local Similarity 32.2%; Pred. No. 7.4e-19;

Matches 96; Conservative 48; Mismatches 152; Indels 2; Gaps 2;

QY 254 ADSTAVNGSIPTDKKIGFLGLMGSGIVGNLLMGHTVTVMNRATKCDLFTQEGARL 313

DB 24 ASSIISDIITPSNTKIGWIGVWGRSMCGHLIKAGYTVVFNRTTSKATQTLIDMGANV 83

QY 314 GRTPAEVSTCDITFACVSDPKAAKDLVLGP -SGVLQGIIRPKGCYVDMSTVDADTVTELA 372

DB 84 ADSPNSVAEQSDVWFTIVGYPDSVRHVLDPKSGALSGLRQGGVLDMTTEPSSLAERIA 143

QY 373 QVIVSRGRFLEAPVSGNQQLSNDQMLVLAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432

DB 144 KAASFKNCFSDAPVSGDGLGAKNKGKLSIFAGGDETTVRKLDPLSLMGKNV-FMGTSK 202

QY 433 AAKMMLVNMVQSGSPMATIAEGLTLAHTVGTGSOQTLILNQQLASIFLDQKCNILQG 492

DB 203 GOFAXLANQITASTMLGIVEGLIYAHKAGLDVKKFLEAISTGAAGSKSIDLYGDRILKR 262

QY 493 NFKPDFYLYKQKQLRLAIALGDVAVNHPTPMAAANEVYKRAKALDOSDNMSAVYRA 550

DB 263 DFDPGFYVNFVKDLGICLNECQRMGLAPGLALAQQLYLSLKAHGEGLGTQALLA 320

RESULT 17

Q97DX8 PRELIMINARY; PRT; 292 AA.

AC Q97DX8

DT 01-OCT-2001 (Tremblrel. 18, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC

DE B.subtilis ortholog.

GN CAC3342.

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI\_TaxID=1488;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE=21359325; PubMed=11466286;

RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Soucaille P., Daly M.J.,

RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

RT "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

DR J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AE007831; AAK81274.1; -

DR PIR; G97310; G97310.

DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. . .); IEA.

DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.

DR InterPro; IPR006183; 6PGD.

DR InterPro; IPR006115; 6PGD NAD.

DR Pfam; PF03446; NAD binding\_2; 1.

DR PRINTS; PR00076; 6FGDHRGNASE.

KW Complete proteome.

SQ SEQUENCE 292 AA; 31542 MW; 7EF0BCC9D59EED87 CRC64;

Query Match 13.1%; Score 375; DB 16; Length 292;

Best Local Similarity 30.0%; Pred. No. 2.6e-18;

Matches 85; Conservative 55; Mismatches 143; Indels 0; Gaps 0;

QY 269 KIGFLGLMGSGIVSNLLMGHTVTVMNRATKCDLFTQEGARLGTTPAEVSTCDITF 328

DB 7 KIGFIGTVMGKGNKMLKGGYTVHYVNTKEKALPLVEIGAVLETISKLSQRCDVII 66

QY 329 ACVSDPKAAKDLVLGPGSVLQGIIRPKGCYVDMSTVDADTVTELAQVIVSRGRLEAPVS 388

DB 67 TWVGYPDSVEEVFNQNGILNKLKQSYVYVVDITTSKPSLAKKIYAAAKERNIFDALPVS 126

QY 389 GNQOLSNDGMVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLIVNMVQSGSFM 448



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Db 127 GGDIGAAEGTSLNMGVGEKFAFDALMPFELMGKNVILQSGAGSGOHTKMCNQIAIASNI 186
QY 449 ATIAEGLTLAHTVGTQSOOTLLDILNOQLASIFLDQKCNILQGNKEKPDFLKYIQKDLR 508
Db 187 MGVCALSYAKKSGNINETVLKSTGAGASWQLSAYAPRLKGDGFPFGYIKHFVKDMK 246
QY 509 LAIALGDVANHPTPMAAANAENVYKRAKALQSDNDMSAVYRAY 551
Db 247 IALBEADEMGLKTPALELSKLYDKLKEGKEDLGTQALYHLY 289

RESULT 18
Q8ZXR3 ID Q8ZXR3 PRELIMINARY; PRT; 284 AA.
AC Q8ZXR3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE1145.
GN PAE1145.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=12664397; PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Muller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
DR EMBL; AE009806; AAL63283.1; -.
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006098; P:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006573; P:valine metabolism; IEA.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PS00076; 6PGDHRGNASE.
DR PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
KW Hypothetical protein; Complete proteome.
SQ SSSEQUENCE 284 AA; 30155 MW; 9D845881717D8550 CRC64;

Query Match 13.0%; Score 373; DB 17; Length 284;
Best Local Similarity 30.2%; Pred. No. 3.5e-18;
Matches 80; Conservative 54; Mismatches 131; Indels 0; Gaps 0;

QY 269 KIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARLGTAEVYSTCDITF 328
Db 2 RVGVGLGIMGGPMAMHLRAGLLAAVYNTRAKAEPEFKLVVAGSPGLAKRVDDVI 61
QY 329 ACVSDPKAAKDLVLGSPGVLIQIRPGKCYVDMSTVDADTVELAQVTSVGRGRFLAPVS 388
Db 62 IMVSDAPDVEQLFGPGGIVEGARPGLIIVDMSTNSPDWARRFAERLAQYGVFELDAPT 121
QY 389 GNQOLSDNGMLVILAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMLIVNMQGSFM 448
Db 122 GGQKGAVEGTLTVWVGKKEELFKRLLPVQAFGNIVYVGVPGVQAMKLVNQVVAALNT 181
QY 449 ATIAEGLTLAHTVGTQSOOTLLDILNOQLASIFLDQKCNILQGNKEKPDFLKYIQKDLR 508
Db 182 VAMVEGRLAKALGLDMKVVQVLTGTGAARSGSIELYLPKLLRGDLTPFGKAAHLKKDLS 241
QY 509 LAIALGDVANHPTPMAAANAENVYK 533
Db 242 YVMELANRASLSLPATALALELYKK 266

RESULT 19

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Q89HA0 ID Q89HA0 PRELIMINARY; PRT; 313 AA.
AC Q89HA0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxidoreductase.
GN BLR6094.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197 (2002).
DR EMBL; AP005957; BAC51359.1; -.
DR GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006098; P:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
DR InterPro; IPR006183; 6PGD.
DR InterPro; IPR006115; 6PGD_NAD.
DR Pfam; PF03446; NAD_binding_2; 1.
DR PRINTS; PR00076; 6PGDHRGNASE.
DR Complete proteome.
SQ SEQUENCE 313 AA; 32732 MW; 3B92612722105D51 CRC64;

Query Match 13.0%; Score 372.5; DB 16; Length 313;
Best Local Similarity 31.2%; Pred. No. 4.3e-18;
Matches 93; Conservative 55; Mismatches 145; Indels 5; Gaps 3;

QY 254 ADSTAVNGSITPTDKKIGFLGLGMSGIVSNLLKMGHTVTVNRTAEKCDLFIQEGARL 313
Db 13 ADASKAN---PQDERFGYGLGLGMPTRLLKAGYQVSNRSGKVVPIVEAGARH 69
QY 314 GRTPAEVYSTCDITFACVSDPKAAKDLVLGSPGVLIQIRPGKCYVDMSTVDADTVELA- 372
Db 70 GASPRDVMAGSDIVFMCVTDAAAEVIFGAEGLSFAPGAGKLVDFSSIFHPDAARDLAT 129
QY 373 QVIVSRGRFLAPVSGNQOLSNDGMLVILAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
Db 130 RLKAANGAGWIDAPVSGGTGAEGLTAIMAGGDASDIERVPRPVLTMARFRTHMGPTGA 189
QY 433 AAKMLIVNMQGSFWATIAEGLTLAHTVGTQSOOTLLDILNOQLASIFLDQKCNILQ 492
Db 190 GQTAKLCNQVIGCANAVLAEATRLAVNAGIDANRLPEALAGGFADSIPQLFVPRVQ 249
QY 493 NFKPDF-YLKYIQKRLALALGDVANHPTPMAAANAENVYKRAKALQSDNDMSAVYR 549
Db 250 IHPPLGHITATMLKDLDTVADVAQTSTPVPMTATLAGQLFLAKAARGADADALEIYK 307

RESULT 20
Q8U2W2 ID Q8U2W2 PRELIMINARY; PRT; 278 AA.
AC Q8U2W2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3-hydroxyisobutyrate dehydrogenase.
GN PF0716.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.

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Thu Sep 16 09:36:52 2004

KW Complete proteome.  
SQ SEQUENCE 301 AA; 31326 MW; 91AC4PBF73F6925F CRC64;

Query Match 12.4%; Score 354.5; DB 16; Length 301;  
Best Local Similarity 29.6%; Pred. No. 7.6e-17;  
Matches 87; Conservative 58; Mismatches 134; Indels 15; Gaps 6;

QY 264 TPTDKKIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKDLFOE-CARLGRTPAEVVS 322  
DB 11 TTTTRNVAFLGLGVNGLPMAGHLARAGHQVTVYNNRTAAQAQAAAEFGKAAATPREAAA 70

QY 323 TCDITFACVSPKAAKDLVLGPGVLOGIRPGKCYVDMSTVDADTVTELAAQVIVSRGGRF 382  
DB 71 GAQIVFCVCGNDLRSVVLGNDGAFAGACAGAFVVDHTTASADVARELYAAARELNQF 130

QY 383 LEAPVSGNQQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGE--VGNAAKM--M 437  
DB 131 IDAPVSGQAGAVNGALTITMCGDSATFEDIKPAHAFAFGRAVTLVGPFGAGLAKMNVQV 190

QY 438 LIVNMVQGSFMATIAEGLTLAHTVGTOSQOTLLDILNOGLASIFLDQKCNILQGNFKPD 497  
DB 191 CIAGVVOG-----LSEALAFGQTAGLDMKLVLDVLSKGAQSQWQVENRGATWDDQDFDG 245

QY 498 FYLKIYQDLRLAIALGAVNHPT--PMAAAANEVYKRAKALDQSDNDMSAVYR 549  
DB 246 FAVDWKRDGLGLVIA--EARNNGARLPLTALVDQFVGVQKMGNGRWDITSSLIK 297

RESULT 29  
Q8ESP3 PRELIMINARY; PRT; 298 AA.

ID Q8ESP3  
AC Q8ESP3; 23, Created)  
DT 01-WAR-2003 (TREMELrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
DE 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).  
GN OB0581.  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=22220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."  
RT Nucleic Acids Res. 30:3927-3935(2002).  
RL EMBL; AF004595; BAC12537.1; -.  
DR GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0004616; P:phosphoglucuronate dehydrogenase (decarboxyla. .; IEA.  
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.  
DR InterPro; IPR006183; 6PGD.  
DR InterPro; IPR006115; 6PGD NAD.  
DR Pfam; PF03446; NAD\_binding\_2; 1.  
DR PRINTS; PR00076; 6PGDHRGNASE.  
KW Oxidoreductase; Complete proteome.  
SQ SEQUENCE 298 AA; 31931 MW; 4D80E5EAAF7C3C74 CRC64;

Query Match 12.3%; Score 353; DB 16; Length 298;  
Best Local Similarity 27.4%; Pred. No. 9.5e-17;  
Matches 77; Conservative 56; Mismatches 148; Indels 0; Gaps 0;

QY 270 IGFLGLMGSGIVSNLLKMGHTVTVNRTAEKDLFOE-CARLGRTPAEVVSCTITFA 329  
DB 9 IGFIGTGVGKSMKKNLNLNAGYSIRIFTRTKSADLLNLNIGAKWDKDIPTLAKQCVIIT 68

QY 330 CVSDPKAAKDLVLGPGVLOGIRPGKCYVDMSTVDADTVTELAAQVIVSRGGRFLEAPVS 389  
DB 69 MVGYPVDEEYVILGEQGLIKCNKGYLIDMTTSKPSLABEIFSVEKHLGLHVLDAFVS 128

QY 390 NQQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449  
DB 129 GDIGAESGTLAINTGGRSVYDVLPIFQVILGENISYQGPAGTQCHTQMSNQIAIASNMI 188

QY 450 TIAGSLTLAHTVGTOSQOTLLDILNOGLASIFLDQKCNILQGNFKPDYLYKYIQKDLRL 509  
DB 189 GVCSESLYAKAGLDLPKVLATISTGAAAASFSLKLGARMLENDENFGYVYKHFIDKMRI 248

QY 510 AIALGDVANHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550  
DB 249 ALESSQAFGLDTPGLKLAIDLYEQLSDMGEDSGTQALIKA 289

RESULT 30  
Q830A7 PRELIMINARY; PRT; 296 AA.

ID Q830A7  
AC Q830A7; 24, Created)  
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE 2-hydroxy-3-oxopropionate reductase.  
GN GLXR OR EP2889.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=V583 / ATCC 700802;  
RX MEDLINE=22550857; PubMed=12663927;  
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seehadri R.,  
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Madupu R., Nelson W.,  
RA Dagherty S., DeBoy R.T., Durkin S., Kolenay J., Shetty J., Khouri H.,  
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Fraser C.M.;  
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;  
RT "Role of mobile DNA in the evolution of vancomycin-resistant Enterococcus faecalis."  
RT Science 299:2071-2074(2003).  
RL EMBL; AF016956; AAC82578.1; -.  
DR TIGR; EF2889; -.  
DR GO; GO:0004616; P:phosphoglucuronate dehydrogenase (decarboxyla. .; IEA.  
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.  
DR InterPro; IPR006183; 6PGD.  
DR InterPro; IPR006115; 6PGD NAD.  
DR Pfam; PF03446; NAD\_binding\_2; 1.  
DR PRINTS; PR00076; 6PGDHRGNASE.  
KW Complete proteome.  
SQ SEQUENCE 296 AA; 31831 MW; 9BBI773D84D7796B CRC64;

Query Match 12.2%; Score 350; DB 16; Length 296;  
Best Local Similarity 29.9%; Pred. No. 1.5e-16;  
Matches 79; Conservative 49; Mismatches 136; Indels 0; Gaps 0;

QY 269 KIGFLGLMGSGIVSNLLKMGHTVTVNRTAEKDLFOE-CARLGRTPAEVVSCTITF 328  
DB 3 KIGFIGTGVGKSIIRNMKNLSNVNRYARTKSTDDLVAEGAVWDTPKAIEASDIIF 62

QY 329 ACVSDPKAAKDLVLGPGVLOGIRPGKCYVDMSTVDADTVTELAAQVIVSRGGRFLEAPVS 388  
DB 63 TMVGFSDVEGVYFNETGTFQADLTGKIVVDLTSTPTLAEKAKKAAAEVGAHALDAPVS 122

QY 389 GNQQLSNDGMLVILAAAGDRGLYEDSCSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448  
DB 123 GGDLAGKNGTLTIMVGDOESYDVLPIFKTFKTLHGSAGKGOHTKMANQIMTAGTM 182

QY 449 ATTAEGTLAHTVGTOSQOTLLDILNOGLASIFLDQKCNILQGNFKPDYLYKYIQKDLR 508  
DB 183 TGUTEMLVYANATGLTEKLVLETVGGGAANSLSNYPRIKLEDYTPGFVKHFIKDLK 242

QY 509 LALALGDVANHPTPMAAAANEVYK 532  
DB 243 IALDEAKKLDPLPATQKATELYE 266

Search completed: September 16, 2004, 07:32:08  
Job time : 54 secs





Title: GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2004, 07:30:42 ; Search time 55 Seconds  
 (without alignments)  
 195.215 Million cell updates/sec

Title: **US-10-067-482-2\_COPY\_271\_308**

Perfect score: 200

Sequence: 1 GFLGLMGSGIVSNLLKMGHTVTVMNRKTAERCDLFQ 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : **A\_Geneseq\_29Jan04.\***

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 200   | 100.0       | 472    | 6     | Aae38240 Human enz |
| 2          | 200   | 100.0       | 553    | 6     | Aao16415 Human nuc |
| 3          | 166   | 83.0        | 547    | 2     | Aaw69240 Clone AQ7 |
| 4          | 166   | 83.0        | 547    | 4     | Aab90720 Human AQ7 |
| 5          | 166   | 83.0        | 550    | 4     | Aau21690 Novel hum |
| 6          | 166   | 83.0        | 550    | 7     | Aac46331 Human neo |
| 7          | 126   | 63.0        | 574    | 4     | Abb60930 Drosophil |
| 8          | 125   | 62.5        | 161    | 7     | Abm74242 DNA clone |
| 9          | 125   | 62.5        | 168    | 3     | Asg41222 Arabidops |
| 10         | 125   | 62.5        | 289    | 3     | Aab19491 Amino aci |
| 11         | 125   | 62.5        | 289    | 6     | Aae36392 A. thalia |
| 12         | 124   | 62.0        | 345    | 5     | Aae19929 Soybean 3 |
| 13         | 123   | 61.5        | 343    | 5     | Aag10424 Arabidops |
| 14         | 123   | 61.5        | 353    | 3     | Aag10423 Arabidops |
| 15         | 118   | 59.0        | 290    | 6     | Aae36391 Tulip pis |
| 16         | 117   | 58.5        | 360    | 5     | Aae19927 Corn 3-hy |
| 17         | 109   | 54.5        | 292    | 6     | Abu24159 Protein e |
| 18         | 106   | 53.0        | 288    | 6     | Abu17331 Protein e |
| 19         | 106   | 53.0        | 299    | 6     | Ada36120 Acinetoba |
| 20         | 105   | 52.5        | 290    | 6     | Abu17066 Protein e |
| 21         | 102   | 51.0        | 326    | 6     | Ada36852 Acinetoba |
| 22         | 101   | 50.5        | 285    | 3     | Aag10425 Arabidops |
| 23         | 100   | 50.0        | 295    | 6     | Abu29967 Protein e |
| 24         | 100   | 50.0        | 299    | 7     | Adc95482 E. faeciu |
| 25         | 93    | 46.5        | 492    | 2     | Aaw27613 Brevibact |

Aag06417 Arabidops  
 Aag06416 Arabidops  
 Aag06415 Arabidops  
 Aag20956 Arabidops  
 Aag20955 Arabidops  
 Aag20954 Arabidops  
 Abb67146 Drosophil  
 Aag41223 Arabidops  
 Abu28970 Protein e  
 Abu19266 Staphyloc  
 Auu34285 Staphyloc  
 Auu36997 Staphyloc  
 Abm71061 Staphyloc  
 Abu15983 Protein e  
 Aag79095 Amino aci  
 Aba48294 Listeria  
 Abu2435 Protein e  
 Aba79369 Corynebact  
 Aab79368 Corynebact  
 Aag91351 C glutam  
 Adc35705 6-phospho  
 Add13347 C. glutam  
 Aay34958 Chlamydia  
 Aba26880 Protein e  
 Abu27221 Protein e  
 Abu26044 Protein e  
 Aab15899 E. coli p  
 Abb91546 Herbicida  
 Abu48551 Protein e  
 Aag41224 Arabidops  
 Abb55570 Lactococc  
 Abb91547 Herbicida  
 Abu21852 Protein e  
 Aae19926 Corn 3-hy  
 Aba49230 Listeria  
 Abu2839 Protein e  
 Abg17598 Novel hum  
 Abu34614 Protein e  
 Auu35461 Haemophil  
 Abb52479 Escherich  
 Abu30295 Protein e  
 Aag81157 Mycobacte  
 Abu36691 Protein e  
 Aau39521 Propionib  
 Abm36040 Propionib  
 Abb52479 Escherich  
 Abu37157 Protein i  
 Abu43488 Protein e  
 Abu39412 Protein e  
 Aag12290 Zea mays  
 Aag26084 Zea mays  
 Aag19126 Zea mays  
 Abu19468 Protein e  
 Abu22158 Protein e  
 Abm73851 DNA clone  
 Ada48242 Rice prot  
 Aay99866 Escherich  
 Abu49748 Protein e  
 Abu36070 Protein e  
 Abu33961 Protein e  
 Aag52190 Arabidops  
 Aag08461 Arabidops  
 Aag82286 S. epider  
 Abu42697 Protein e  
 Abp38396 Staphyloc  
 Abu21583 Protein e  
 Abu31389 Protein e  
 Auu55660 Protein e  
 Aay99857 Escherich  
 Auu38229 Salmonell  
 Abu48164 Protein e  
 Aag16834 Arabidops  
 Aag16833 Arabidops

99 73 36.5 192 3 AAY99862 Aay99862 Escherich  
100 73 36.5 298 7 ADD95220 Add95220 Alcaligen

ALIGNMENTS

RESULT 1  
AAE38240  
ID AAE38240 standard; protein; 472 AA.

AC AAE38240;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human enzyme (ENZM) protein #32.  
XX  
XX Human; enzyme; ENZM; immune disorder; infection; myocardial infarction;  
KW gene therapy; anaemia; acquired immune deficiency syndrome; infection;  
KW reproductive disorder; cardiovascular; eye; cell proliferation; cancer;  
KW AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence;  
KW infertility; atherosclerosis; metabolic disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO2003052075-A2.  
PN  
XX 26-JUN-2003.  
PD  
XX 12-DEC-2002; 2002WO-US040161.  
PF  
XX 14-DEC-2001; 2001US-0340357P.  
PR  
XX 20-DEC-2001; 2001US-0342962P.  
PR  
XX 21-DEC-2001; 2001US-0343558P.  
PR  
XX 22-JAN-2002; 2002US-0351107P.  
PR  
XX (INCY-) INCYTE GENOMICS INC.  
PA

XX Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R;  
PI Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;  
PI Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis JP;  
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;  
XX  
XX WPI: 2003-533016/50.  
DR  
XX N-PSDB; AAD57520.  
DR  
XX  
XX New human enzyme (ENZM) polypeptide, useful for preparing a composition  
PT for treating a disease associated with decreased expression or  
PT overexpression of ENZM e.g. cancer.  
XX  
XX Claim 1; Page 298-299; 264pp; English.

XX The invention relates to human enzyme (ENZM) polypeptides and their  
CC corresponding polynucleotides. ENZM sequences are useful for preparing a  
CC composition for diagnosing or treating a disease or condition associated  
CC with decreased expression or overexpression of functional ENZM. The  
CC disorders include immune disorders (anaemia, allergy or asthma),  
CC infectious disorders (viral, fungal, parasitic or protozoal infection),  
CC immune deficiencies (acquired immune deficiency syndrome; AIDS),  
CC metabolic disorder (Addison's disease, diabetes or goitre), reproductive  
CC disorders (infertility or impotence), cardiovascular disorders  
CC (atherosclerosis or myocardial infarction), eye disorders and cell  
CC proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The  
CC present sequence is human ENZM protein  
XX  
XX Sequence 472 AA;

Query Match 100.0%; Score 200; DB 6; Length 472;  
Best Local Similarity 100.0%; Pred. No. 4.3e-20;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFLGLGLMGSGIVSNLLKMGHTVTWNRATKCDLFIQ 38  
|||||

Db 190 GFLGLGLMGSGIVSNLLKMGHTVTWNRATKCDLFIQ 227

RESULT 2  
AAO16415  
ID AAO16415 standard; protein; 553 AA.

XX AAO16415;  
XX  
XX 10-APR-2003 (first entry)  
XX  
XX Human nucleic acid-associated protein (NAAP) - SEQ ID No 12.

XX  
XX Human; nucleic acid-associated protein; NAAP; arteriosclerosis;  
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS;  
KW cancer; developmental disorder; renal tubular acidosis; anaemia; asthma;  
KW mental retardation; neurological disorder; Alzheimer's disease; epilepsy;  
KW Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy;  
KW Crohn's disease; transgenic animal; animal model.  
XX  
XX Homo sapiens.  
OS  
XX WO2003000864-A2.  
PN  
XX 03-JAN-2003.  
PD  
XX 20-JUN-2002; 2002WO-US021179.  
PF  
XX 22-JUN-2001; 2001US-0300518P.  
PR  
XX 29-JUN-2001; 2001US-0301787P.  
PR  
XX 29-JUN-2001; 2001US-0301792P.  
PR  
XX 29-JUN-2001; 2001US-0301892P.  
PR  
XX 06-JUL-2001; 2001US-0301893P.  
PR  
XX 06-JUL-2001; 2001US-0303405P.  
PR  
XX 06-JUL-2001; 2001US-0303442P.  
PR  
XX 15-MAR-2002; 2002US-0364438P.  
PR  
XX (INCY-) INCYTE GENOMICS INC.

XX Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM;  
PI Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ;  
PI Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR;  
PI Borowsky ML, Yao MG, Walia NK, Bandnan O, Lal PG, Becha SD, Lee SY;  
PI Richardson TW, Elliott VS, Luo W, Tang Y, Zebajradian Y, Lu Y;  
XX  
XX WPI: 2003-201420/19.  
DR  
XX N-PSDB; AAL51565.  
DR  
XX New nucleic acid-associated proteins and polynucleotides, useful for  
PT diagnosing, treating or preventing cell proliferative (e.g. cancer),  
PT neurological (e.g. epilepsy or Parkinson's disease), or autoimmune  
PT disorders (e.g. AIDS).  
XX  
XX Claim 1; Page 227-228; 312pp; English.

XX The invention comprises the amino acid and coding sequences of human  
CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of  
CC the invention are useful for diagnosing, treating or preventing disorders  
CC associated with aberrant expression of NAAP, such as: cell proliferative  
CC disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis  
CC or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia  
CC or mental retardation); neurological disorders (e.g. Alzheimer's disease,  
CC Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders  
CC (e.g. AIDS, allergies, asthma or Crohn's disease). The DNA sequences of  
CC the invention are useful for creating transgenic animals to model human  
CC disease. The present amino acid sequence represents a human nucleic acid-  
CC associated protein of the invention  
XX  
XX Sequence 553 AA;

Query Match 100.0%; Score 200; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 5.2e-20;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFQ 38  
 DE 271 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEKCDLFQ 308

RESULT 3  
 AA69240  
 ID AAW69240 standard; protein; 547 AA.

AC AAW69240;  
 DT 21-OCT-1998 (first entry)  
 XX

DE Clone AQ73\_3 protein sequence.

KW Secreted protein; nutritional source; cell proliferation activity;  
 KW cell differentiation activity; immune stimulant; tissue growth activator;  
 KW haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor;  
 KW tumour inhibitor; clone AQ73\_3.

XX Homo sapiens.  
 OS  
 XX  
 PN W09825962-A2.  
 XX

PD 18-JUN-1998.

PF 12-DEC-1997; 97WO-US023224.

XX 13-DEC-1996; 96US-00766263.

PR 11-DEC-1997; 97US-00989232.

XX (GEMY ) GENETICS INST INC.

PA

PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

XX Spaulding V, Agostino MJ;

DR WPI; 1998-362424/31.

XX N-PSDB; AAV44859.

XX New isolated polynucleotides - obtained from human adult testis, human

PT adult ovary, human adult brain and human adult heart cDNA libraries.

PS Claim 15; Page 66-67; 108pp; English.

XX This sequence is secreted protein, encoded by a polynucleotide of the  
 CC invention. The DNA was isolated from a human adult ovary cDNA library,  
 CC and is designated clone AQ73\_3. The DNA sequences and encoded  
 CC polypeptides can be used as nutritional sources or supplements, or may  
 CC exhibit e.g. cytokine and cell proliferation/differentiation activity,  
 CC immune stimulating or suppressing activity, haematopoiesis regulating  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC activin/inhibin activity, chemostatic/chemokinetic activity,  
 CC cadherin/tumour invasion suppressor activity, tissue growth activity,  
 CC tumour inhibition activity or other activities

XX Sequence 547 AA;

Query Match 83.0%; Score 166; DB 2; Length 547;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEK 32  
 DE 271 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEK 302

RESULT 4  
 AAB90720  
 ID AAB90720 standard; protein; 547 AA.

XX

AC AAB90720;

XX

DT 07-JUN-2001 (first entry)

XX Human AQ73\_3 protein sequence SEQ ID 137.

DE Human; secreted protein; nutrient; cytokine modulator; proliferation;  
 KW differentiation; immune system modulator; tissue growth; chemotactic;  
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;  
 KW haematopoiesis.

XX Homo sapiens.

OS WO200119988-A1.

PN 22-MAR-2001.

PD 14-SEP-2000; 2000WO-US025135.

XX 17-SEP-1999; 99US-00398829.

XX (GEMY ) GENETICS INST INC.

PA

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

DR WPI; 2001-244801/25.

XX N-PSDB; AAF98456.

PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.

XX cytokine and cell proliferation/differentiation activity, the immune

PS system and hematopoiesis regulating activity.

XX Disclosure; Page 468-470; 557pp; English.

CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
 CC proteins AAB30667 - AAB90750. The cDNA clones are isolated from various  
 CC tissue types, and may be used in the prevention, treatment and diagnosis  
 CC of diseases associated with inappropriate protein expression. The  
 CC polypeptides and nucleic acids may be used as nutrients or to modulate  
 CC cytokine and cell proliferation/differentiation activity and may also be  
 CC involved in modulation of the immune system. The cDNA sequences,  
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis  
 CC regulating activity; tissue growth activity; activin/inhibin activity;  
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis  
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
 CC activity. Included in the invention are probes represented in AAF98490 -  
 CC AAF98572 which are specific for the cDNA clones encoding the secreted  
 CC proteins

XX Sequence 547 AA;

Query Match 83.0%; Score 166; DB 4; Length 547;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEK 32  
 DE 271 GFLGLMGSGIVSNLLKMGHTVTWNRRTAEK 302

RESULT 5

AAU21690

ID AAU21690 standard; protein; 550 AA.

XX

AC AAU21690;

XX

DT 04-DEC-2001 (first entry)

XX

DE Novel human neoplastic disease associated polypeptide #123.

XX

KW Human; neoplastic disease associated polypeptide; cancer;  
 KW hyperproliferative disorder; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;



PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465558/50.  
XX N-PSDB; AAS34889.  
XX  
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to  
PT diagnose diseases or disorders associated with aberrant expression or  
PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.  
XX  
XX Claim 11; SEQ ID NO 417; 687pp; English.  
XX  
CC The present invention relates to the isolation of novel human neoplastic  
CC disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA  
CC sequences encoding for these polypeptides. The sequences of the invention  
CC are useful in the diagnosis, treatment, prevention and/or prognosis of  
CC disorders involving neoplastic disease such as hyperproliferative  
CC disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem  
CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or  
CC Hodgkin's lymphoma). The sequences of the invention may also be useful  
CC for treating other disorders such as neural disorders, immune system  
CC disorders, muscular disorders, reproductive disorders, gastrointestinal  
CC disorders, pulmonary disorders, cardiovascular disorders and renal  
CC disorders. The polynucleotide sequences of the invention are also useful  
CC in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic  
CC disease associated polypeptides of the invention. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 550 AA;  
XX  
XX Query Match 83.0%; Score 166; DB 4; Length 550;  
XX Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GFLGLGMSGIVSNLLKMGHTVTVMNRATK 32  
XX |||||  
XX Db 274 GFLGLGMSGIVSNLLKMGHTVTVMNRATK 305  
XX  
XX RESULT 6  
XX ADC46331  
XX ID ADC46331 standard; protein; 550 AA.  
XX AC ADC46331;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
XX DE Human neoplastic disease-associated gene 123 protein #1.  
XX  
XX KW Neoplastic disease-associated polypeptide; gene therapy;  
XX hyperproliferative disease; cancer; autoimmune disorder; diabetes;  
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
XX autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;  
XX haematologic disorder; anaemia; thrombocytopenia; allergic reaction;  
XX asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;  
XX inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;  
XX Alzheimer's disease; Parkinson's disease; renal disease;  
XX acute glomerulonephritis; end-stage renal disease;  
XX cardiovascular disorder; atherosclerosis; myocarditis;  
XX infectious disease; AIDS; cachexia; anorexia; wound healing;  
XX epithelial cell proliferation; Human.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2003082758-A1.  
XX  
XX PD 01-MAY-2003.  
XX

PF 22-MAR-2002; 2002US-00103313.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
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PR 27-SEP-2000; 2000US-0235836P.  
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PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.



XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL161176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB5773-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 574 AA;

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Query Match 63.0%; Score 126; DB 4; Length 574;
Best Local Similarity 60.5%; Pred. No. 2.8e-09;
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0

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RESULT 8  
ABM74242  
ID ABM74242 standard; protein; 161 AA.  
XX  
XX  
AC ABM74242;  
XX  
XX  
DT 17-OCT-2003 (first entry)  
XX  
XX  
DE DNA clone originating in barley containing SNP sequence #652.  
XX  
XX  
KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.  
XX

|    |                                                                     |
|----|---------------------------------------------------------------------|
| XX | Hordeum vulgare.                                                    |
| OS |                                                                     |
| XX | WO2003057877-A1.                                                    |
| XX |                                                                     |
| XX | 17-JUL-2003.                                                        |
| XX |                                                                     |
| XX | 16-DEC-2002; 2002WO-IB005403.                                       |
| XX |                                                                     |
| XX | 20-DEC-2001; 2001JP-00387059.                                       |
| PR | 20-DEC-2001; 2001JP-00387131.                                       |
| PR | 20-DEC-2001; 2001JP-00403299.                                       |
| PR | 20-DEC-2001; 2001JP-00403300.                                       |
| PR | 27-SEP-2002; 2002JP-00327515.                                       |
| XX |                                                                     |
| XX | (UYN1-) UNIV JAPAN OKAYAMA.                                         |
| XX |                                                                     |
| XX | Sato K, Takeda K, Kohara Y;                                         |
| PI |                                                                     |
| XX | WPI; 2003-587127/55.                                                |
| XX |                                                                     |
| XX | Single nucleotide polymorphism sites in barley varieties and DNA    |
| PT | sequences containing them for analysis and identification of barley |
| PT | varieties and production of barley transformants with desired       |
| PT | characteristics.                                                    |
| PT |                                                                     |

Disclosure; SEQ ID XX; 284pp; Japanese.

The present invention relates to oligonucleotide clones originating in barley (*Hordeum vulgare*) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published-pct-sequences](http://wipo.int/pub/published-pct-sequences)

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XX XX Sequence 161 AA;
SQ
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Best Local Similarity 64.7%; Pred. No. 8.1e-10;
Matches 22; Conservative 5; Mismatches -7; Indels 0; Gaps 0;
QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRRTABKCD 34
Db |||||::: : |||| : ||||| |||
 48 GFLGLGIMGAPWASNLIKAGCDITVWNRTSKCD 81

RESULT 9
AAG41222
ID AAG41222 standard; protein; 168 AA.
XX AC AAG41222;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 51261.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
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PR 23-MAR-1999; 99US-0123548P.
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PR 03-JUN-1999; 99US-0137222P.
PR 04-JUN-1999; 99US-0137528P.
PR 07-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.

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XX 19-FEB-2002.
PD 29-JUL-1999; 99US-00364230.
PF 31-JUL-1998; 98US-0094950P.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;
XX WPI; 2002-204621/26.
XX N-PSDB; AAD31750.
XX Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used
XX to produce transgenic plants having an altered expression of the enzyme.
XX Claim 1; Col 33-36; 40pp; English.
XX The invention relates to nucleic acid fragments encoding branched chain
XX amino acid degradation enzymes. Particularly the invention relates to 3-
XX hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA)
XX lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides
XX derived from corn, rice and wheat. Sequences of the invention are used to
XX produce transgenic plants having an altered expression of the enzyme.
XX Polynucleotides of the invention can be used as probes for physical
XX mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate
XX dehydrogenase (EC 1.1.1.31) from seq2w.pk0002.e5 clone
XX Sequence 345 AA;
XX
XX Query Match 62.0%; Score 124; DB 5; Length 345;
XX Best Local Similarity 64.9%; Pred. No. 2.9e-09;
XX Matches 24; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
QY 1 GFLGLGMSGIGVSNLLKMGHVTWNRTAEKCDLFI 37
DB 55 GFLGLGMSGPMHNLKAGVDLTVWNRKSKCDPLI 91
RESULT 13
AAG10424
ID AAG10424 standard; protein; 343 AA.
AC AAG10424;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 8740.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
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| PR | 26-AUG-1999; | 99US-0150566P   |
| PR | 27-AUG-1999; | 99US-0150884P   |
| PR | 27-AUG-1999; | 99US-0151065P   |
| PR | 30-AUG-1999; | 99US-0151066P   |
| PR | 31-SEP-1999; | 99US-0151303P   |
| PR | 01-SEP-1999; | 99US-0151438P   |
| PR | 07-SEP-1999; | 99US-0151930P   |
| PR | 07-SEP-1999; | 99US-0152363P   |
| PR | 13-SEP-1999; | 99US-0153070P   |
| PR | 16-SEP-1999; | 99US-0153758P   |
| PR | 16-SEP-1999; | 99US-0154018P   |
| PR | 20-SEP-1999; | 99US-0154039P   |
| PR | 22-SEP-1999; | 99US-0154779P   |
| PR | 23-SEP-1999; | 99US-0155139P   |
| PR | 24-SEP-1999; | 99US-0155486P   |
| PR | 28-SEP-1999; | 99US-0156559P   |
| PR | 04-OCT-1999; | 99US-0156458P   |
| PR | 04-OCT-1999; | 99US-0157117P   |
| PR | 05-OCT-1999; | 99US-015753P    |
| PR | 06-OCT-1999; | 99US-0157865P   |
| PR | 07-OCT-1999; | 99US-0158023P   |
| PR | 08-OCT-1999; | 99US-0158232P   |
| PR | 12-OCT-1999; | 99US-0158369P   |
| PR | 13-OCT-1999; | 99US-0159233P   |
| PR | 13-OCT-1999; | 99US-0159294P   |
| PR | 14-OCT-1999; | 99US-0159295P   |
| PR | 14-OCT-1999; | 99US-0159330P   |
| PR | 14-OCT-1999; | 99US-0159330P   |

|    |              |                |
|----|--------------|----------------|
| PR | 14-OCT-1999; | 99US-01593311P |
| PR | 14-OCT-1999; | 99US-01593637P |
| PR | 14-OCT-1999; | 99US-01596388P |
| PR | 18-OCT-1999; | 99US-01595884P |
| PR | 21-OCT-1999; | 99US-0160741P  |
| PR | 21-OCT-1999; | 99US-0160767P  |
| PR | 21-OCT-1999; | 99US-0160768P  |
| PR | 21-OCT-1999; | 99US-0160770P  |
| PR | 21-OCT-1999; | 99US-0160814P  |
| PR | 21-OCT-1999; | 99US-0160815P  |
| PR | 22-OCT-1999; | 99US-0160980P  |
| PR | 22-OCT-1999; | 99US-01609891P |
| PR | 22-OCT-1999; | 99US-01609892P |
| PR | 25-OCT-1999; | 99US-0161404P  |
| PR | 25-OCT-1999; | 99US-0161405P  |
| PR | 25-OCT-1999; | 99US-0161406P  |
| PR | 26-OCT-1999; | 99US-0161359P  |
| PR | 26-OCT-1999; | 99US-0161360P  |
| PR | 26-OCT-1999; | 99US-0161361P  |
| PR | 28-OCT-1999; | 99US-0161920P  |
| PR | 28-OCT-1999; | 99US-0161992P  |
| PR | 28-OCT-1999; | 99US-0161993P  |
| PR | 29-OCT-1999; | 99US-0162142P  |

Query Match 61.5%; Score 123; DB 3; Length 343;  
Best Local Similarity 64.7%; Pred. No. 4e-09;

|         |     |              |    |            |    |        |    |      |    |
|---------|-----|--------------|----|------------|----|--------|----|------|----|
| Matches | 22; | Conservative | 4; | Mismatches | 8; | Indels | 0; | Gaps | 0; |
|---------|-----|--------------|----|------------|----|--------|----|------|----|

Qy 1 GFLGLGIMSGSIVSNLLKMGHTVTWNRRTAEKCD 34  
|||||: : |||: | ||||| |||  
Db 55 GFLLGIMSGSPMAQLNIKAGCDVTWNRRTKSICD 88

## RESUIT 14

RESOL 14  
AAG10423  
ID AAG10423 standard; protein; 353 AA.

AC AAG10423;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEO ID NO: 8739.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

06-SEP-2000.

25-FEB-2000: 2000EP-00301439

PR 25-FEB-1999: 99US-0121825D

03-MAR-1999; 99US-0123180P;  
09-MAR-1999; 99US-0123548P

PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999. 99US-0126264D

PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127463D

PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0130714P.

PR 16-APR-1999; 99US-0129845P.  
PR 18-APR-1999; 99US-0129845P.  
PR 18-APR-1999; 99US-0129845P.

PR 21-APR-1999; 99US-0130449P.  
PR 22-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132484P.

|    |              |                |    |              |                |
|----|--------------|----------------|----|--------------|----------------|
| PR | 05-MAY-1999; | 99US-0132485P. | PR | 22-JUL-1999; | 99US-0145087P. |
| PR | 06-MAY-1999; | 99US-0132486P. | PR | 22-JUL-1999; | 99US-0145089P. |
| PR | 06-MAY-1999; | 99US-0132487P. | PR | 22-JUL-1999; | 99US-0145192P. |
| PR | 07-MAY-1999; | 99US-0132863P. | PR | 23-JUL-1999; | 99US-0145145P. |
| PR | 11-MAY-1999; | 99US-0134256P. | PR | 23-JUL-1999; | 99US-0145218P. |
| PR | 14-MAY-1999; | 99US-0134218P. | PR | 23-JUL-1999; | 99US-0145224P. |
| PR | 14-MAY-1999; | 99US-0134219P. | PR | 26-JUL-1999; | 99US-0145276P. |
| PR | 14-MAY-1999; | 99US-0134221P. | PR | 27-JUL-1999; | 99US-0145913P. |
| PR | 14-MAY-1999; | 99US-0134370P. | PR | 27-JUL-1999; | 99US-0145918P. |
| PR | 18-MAY-1999; | 99US-0134768P. | PR | 27-JUL-1999; | 99US-0145919P. |
| PR | 19-MAY-1999; | 99US-0134941P. | PR | 28-JUL-1999; | 99US-0145951P. |
| PR | 20-MAY-1999; | 99US-0135124P. | PR | 02-AUG-1999; | 99US-0146386P. |
| PR | 20-MAY-1999; | 99US-0135353P. | PR | 02-AUG-1999; | 99US-0146388P. |
| PR | 24-MAY-1999; | 99US-0135629P. | PR | 02-AUG-1999; | 99US-0146389P. |
| PR | 25-MAY-1999; | 99US-0136021P. | PR | 03-AUG-1999; | 99US-0147038P. |
| PR | 27-MAY-1999; | 99US-0136392P. | PR | 04-AUG-1999; | 99US-0147204P. |
| PR | 28-MAY-1999; | 99US-0136782P. | PR | 05-AUG-1999; | 99US-0147192P. |
| PR | 01-JUN-1999; | 99US-0137222P. | PR | 05-AUG-1999; | 99US-0147260P. |
| PR | 03-JUN-1999; | 99US-0137528P. | PR | 06-AUG-1999; | 99US-0147303P. |
| PR | 04-JUN-1999; | 99US-0137502P. | PR | 06-AUG-1999; | 99US-0147416P. |
| PR | 07-JUN-1999; | 99US-0137724P. | PR | 09-AUG-1999; | 99US-0147493P. |
| PR | 08-JUN-1999; | 99US-0138094P. | PR | 09-AUG-1999; | 99US-0147935P. |
| PR | 10-JUN-1999; | 99US-0138540P. | PR | 09-AUG-1999; | 99US-0148171P. |
| PR | 10-JUN-1999; | 99US-0138847P. | PR | 10-AUG-1999; | 99US-0148319P. |
| PR | 14-JUN-1999; | 99US-0139119P. | PR | 11-AUG-1999; | 99US-0148341P. |
| PR | 16-JUN-1999; | 99US-0139452P. | PR | 12-AUG-1999; | 99US-0148565P. |
| PR | 16-JUN-1999; | 99US-0139453P. | PR | 13-AUG-1999; | 99US-0148684P. |
| PR | 17-JUN-1999; | 99US-0139492P. | PR | 13-AUG-1999; | 99US-0149368P. |
| PR | 18-JUN-1999; | 99US-0139454P. | PR | 16-AUG-1999; | 99US-0149175P. |
| PR | 18-JUN-1999; | 99US-0139455P. | PR | 17-AUG-1999; | 99US-0149426P. |
| PR | 18-JUN-1999; | 99US-0139456P. | PR | 18-AUG-1999; | 99US-0149722P. |
| PR | 18-JUN-1999; | 99US-0139457P. | PR | 20-AUG-1999; | 99US-0149723P. |
| PR | 18-JUN-1999; | 99US-0139458P. | PR | 20-AUG-1999; | 99US-0149923P. |
| PR | 18-JUN-1999; | 99US-0139459P. | PR | 21-AUG-1999; | 99US-0149902P. |
| PR | 18-JUN-1999; | 99US-0139460P. | PR | 23-AUG-1999; | 99US-0149930P. |
| PR | 18-JUN-1999; | 99US-0139461P. | PR | 25-AUG-1999; | 99US-0150566P. |
| PR | 18-JUN-1999; | 99US-0139462P. | PR | 26-AUG-1999; | 99US-0150884P. |
| PR | 18-JUN-1999; | 99US-0139463P. | PR | 27-AUG-1999; | 99US-0151065P. |
| PR | 18-JUN-1999; | 99US-0139750P. | PR | 27-AUG-1999; | 99US-0151066P. |
| PR | 18-JUN-1999; | 99US-0139763P. | PR | 27-AUG-1999; | 99US-0151080P. |
| PR | 21-JUN-1999; | 99US-0139817P. | PR | 27-AUG-1999; | 99US-0151303P. |
| PR | 21-JUN-1999; | 99US-0139899P. | PR | 30-AUG-1999; | 99US-0151438P. |
| PR | 23-JUN-1999; | 99US-0140353P. | PR | 31-AUG-1999; | 99US-0151930P. |
| PR | 23-JUN-1999; | 99US-0140354P. | PR | 01-SEP-1999; | 99US-0152363P. |
| PR | 23-JUN-1999; | 99US-0140695P. | PR | 07-SEP-1999; | 99US-0153070P. |
| PR | 24-JUN-1999; | 99US-0140823P. | PR | 10-SEP-1999; | 99US-0153758P. |
| PR | 28-JUN-1999; | 99US-0140991P. | PR | 13-SEP-1999; | 99US-0154018P. |
| PR | 29-JUN-1999; | 99US-0142803P. | PR | 15-SEP-1999; | 99US-0154037P. |
| PR | 30-JUN-1999; | 99US-0141287P. | PR | 16-SEP-1999; | 99US-0154779P. |
| PR | 01-JUL-1999; | 99US-0141842P. | PR | 20-SEP-1999; | 99US-0155139P. |
| PR | 01-JUL-1999; | 99US-0142154P. | PR | 22-SEP-1999; | 99US-0155486P. |
| PR | 02-JUL-1999; | 99US-0142055P. | PR | 24-SEP-1999; | 99US-0155659P. |
| PR | 06-JUL-1999; | 99US-0142390P. |    |              |                |

|           |                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| CC        | or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue                                                                                                                                                                              |
| XX        | Sequence 290 AA;                                                                                                                                                                                                                                                                                                                                                                                                                             |
| SQ        | Query Match<br>Best Local Similarity 59.0%; Score 118; DB 6; Length 290;<br>Matches 21; Conservative 5; Mismatches 11; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                     |
| QY        | 1 GFGLGLMGSGIVSNLLKMGHTVTVMNRTAEKCDLFIQ 38<br>     : : : :      : : : :      : : : :      : : : :                                                                                                                                                                                                                                                                                                                                            |
| Db        | 4 GFGLGLMGKAMAVNLLRSGRFVTVWNRITLTKCNELLE 41<br>     : : : :      : : : :      : : : :      : : : :                                                                                                                                                                                                                                                                                                                                           |
| RESULT 16 |                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| AAE19927  |                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ID        | AAE19927 standard; protein; 360 AA.                                                                                                                                                                                                                                                                                                                                                                                                          |
| XX        | AAE19927;                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| AC        | 18-JUN-2002 (first entry)                                                                                                                                                                                                                                                                                                                                                                                                                    |
| DT        | Corn 3-hydroxyisobutyrate dehydrogenase #2.                                                                                                                                                                                                                                                                                                                                                                                                  |
| DE        | Branched chain amino acid degradation enzyme; HM-CoA lyase;                                                                                                                                                                                                                                                                                                                                                                                  |
| XX        | 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;                                                                                                                                                                                                                                                                                                                                                                             |
| KW        | Isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31.                                                                                                                                                                                                                                                                                                                                                                           |
| KW        | Zea mays.                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| OS        | US6348339-B1.                                                                                                                                                                                                                                                                                                                                                                                                                                |
| XX        | 19-FEB-2002.                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PN        | 29-JUL-1999; 99US-00364230.                                                                                                                                                                                                                                                                                                                                                                                                                  |
| XX        | 31-JUL-1998; 98US-0094990P.                                                                                                                                                                                                                                                                                                                                                                                                                  |
| PF        | (DUPO ) DU PONT DE NEMOURS & CO E I.                                                                                                                                                                                                                                                                                                                                                                                                         |
| XX        | Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;                                                                                                                                                                                                                                                                                                                                                                                                  |
| PI        | WPI; 2002-204621/26.                                                                                                                                                                                                                                                                                                                                                                                                                         |
| XX        | N-PSDB; AAD31748.                                                                                                                                                                                                                                                                                                                                                                                                                            |
| DR        | Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.                                                                                                                                                                                                                                                                                           |
| XX        | Claim 1; Col 27-30; 40pp; English.                                                                                                                                                                                                                                                                                                                                                                                                           |
| PS        | The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HM-CoA) lyase and isovaleryl-CoA dehydrogenase polyptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. |
| CC        | Polyclonates of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from crin.pk0191.b10, p0076.cwhan08r and p0118.chsbe01r clones                                                                                                                                                                                                            |
| CC        | p0118.chsbe01r clones                                                                                                                                                                                                                                                                                                                                                                                                                        |
| XX        | Sequence 360 AA;                                                                                                                                                                                                                                                                                                                                                                                                                             |
| SQ        | Query Match<br>Best Local Similarity 58.5%; Score 117; DB 5; Length 360;<br>Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                      |
| QY        | 1 GFGLGLMGSGIVSNLLKMGHTVTVMNRTAEKC 33<br>     : : : :      : : : :      : : : :      : : : :                                                                                                                                                                                                                                                                                                                                                 |
| Db        | 69 GFGLGLMGKAMATNLLRHGFRVTVWNRITLAK 101<br>     : : : :      : : : :      : : : :      : : : :                                                                                                                                                                                                                                                                                                                                               |

|  |             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|--|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|  | CC          | or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|  | XX          | Sequence 290 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|  | SQ          | Query Match<br>Best Local Similarity 59.0%; Score 118; DB 6; Length 290;<br>Matches 21; Conservative 5; Mismatches 11; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|  | OY          | 1 GFGLGIMGSGIVSNLLKMGHTVTVMNRATKCDLFIQ 38<br>     ::   :     :         :: :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|  | Dd          | 4 GFGLGIMGMKAAMVNLRSRFRVTVMNRTLSKNELLE 41<br>     ::   :     :         :: :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|  | RESULT 16   | AEEI9927<br>ID AAEI9927 standard; protein; 360 AA.<br>XX AC AAEI9927;<br>DT 18-JUN-2002 (first entry)<br>DE Corn 3-hydroxyisobutyrate dehydrogenase #2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|  | KW          | Branched chain amino acid degradation enzyme; HMG-CoA lyase;<br>KW 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;<br>KW Isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC I.1.1.31.<br>OS Zea mays.<br>XX US6348339-B1.<br>PN 19-FEB-2002.<br>PD 29-JUL-1999; 99US-00364230.<br>PF 31-JUL-1998; 98US-0094990P.<br>PR (DUPO ) DU PONT DE NEMOURS & CO E I.<br>PI Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;<br>XX WPI; 2002-204621/26.<br>DR N-PSTDB; AAD31748.<br>XX Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.<br>PT Claim 1; Col 27-30; 40pp; English.<br>PS The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA) lyase and isovaleryl-CoA dehydrogenase polyptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC I.1.1.31) from crin.pk0191.b10, p0076.cwhan08r and p0118.chshe01r clones<br>XX Sequence 360 AA;                                                                                                                                                                                   |
|  | OY          | Query Match<br>Best Local Similarity 58.5%; Score 117; DB 5; Length 360;<br>Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|  | Dd          | 1 GFGLGIMGSGIVSNLLKMGHTVTVMNRATKCDLFC 33<br>     ::   :     :         :: :<br>69 GFGLGIMGMKAAMVNLRSRFRVTVMNRTLSKNELLE 101                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|  | P           | 21-OCT-1999; 99US-0160770P.<br>PR 21-OCT-1999; 99US-0160814P.<br>PR 21-OCT-1999; 99US-0160815P.<br>PR 22-OCT-1999; 99US-0160980P.<br>PR 22-OCT-1999; 99US-0160981P.<br>PR 22-OCT-1999; 99US-0160989P.<br>PR 25-OCT-1999; 99US-0161404P.<br>PR 25-OCT-1999; 99US-0161405P.<br>PR 25-OCT-1999; 99US-0161406P.<br>PR 26-OCT-1999; 99US-0161359P.<br>PR 26-OCT-1999; 99US-0161360P.<br>PR 26-OCT-1999; 99US-0161361P.<br>PR 28-OCT-1999; 99US-0161920P.<br>PR 28-OCT-1999; 99US-0161992P.<br>PR 28-OCT-1999; 99US-0161993P.<br>PR 29-OCT-1999; 99US-0162142P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|  | QUERY MATCH | Score 61.5%; DB 3; Length 353;<br>Best Local Similarity 64.7%; Pred.No. 4.1e-09;<br>Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|  | OY          | 1 GFGLGIMGSGIVSNLLKMGHTVTVMNRATKCD 34<br>     ::   :     :         ::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|  | Dd          | 65 GFGLGIMGSPMAQLIKAGCDVTMNRATSKCD 98<br>     ::   :     :         ::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|  | RESULT 15   | AEEI9927<br>ID AAEI9927 standard; protein; 290 AA.<br>XX AC AAEI9927;<br>DT 26-JUN-2003 (first entry)<br>DE Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue.<br>XX Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;<br>KW enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase;<br>KW gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant.<br>OS Tulip pistil.<br>XX WO2002101013-A2.<br>PN 19-DEC-2002.<br>PP 10-JUN-2002; 2002WO-USO18230.<br>PX 08-JUN-2001; 2001US-0297198P.<br>PY (DUPO ) DU PONT DE NEMOURS & CO E I.<br>PZ (PRAB/) PRABHU V.<br>QA Damude HG, Flint D, Prabhu V, Wang H;<br>QB WPI; 2003-201331/19.<br>QC N-PSTDB; AAD55024.<br>XD Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway intermediates.<br>XE Claim 4; Page 110-111; 71pp; English.<br>XF The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrogenase and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alpha-methylene-gamma-aminobutyrate or alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunize animals to produce polyclonal |



CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 288 AA;

Query Match 53.0%; Score 106; DB 6; Length 288;  
 Best Local Similarity 55.6%; Pred. No. 9.2e-07;  
 Matches 20; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 FLGLGLMGSGIVSNLLKMGHTVTWNRATKCDLFI 37  
 DB 11 FLGLGLMGSRMASRLIQAGFQVAVWNRATACEELI 46

RESULT 19  
 ADA36120  
 ID ADA36120 standard; protein; 299 AA.

XX AC ADA36120;

DT 20-NOV-2003 (first entry)

DE Acinetobacter baumannii protein #3281.

KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;  
 KW plant biocontrol agent.

OS Acinetobacter baumannii.

PN US6562958-B1.

PD 13-MAY-2003.

PF 04-JUN-1999; 99US-00328352.

PR 09-JUN-1998; 98US-0088701P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton G, Bush D;

DR WPI; 2003-576092/54.

DR N-PSDB; ADA31994.

XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
 PT for diagnosing a bacterial disease, as components of antibacterial  
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
 PT plants.

PS Example; SEQ ID NO 7407; 328pp; English.

XX The invention relates to isolated Acinetobacter baumannii nucleic acids.  
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
 CC for diagnosing a bacterial disease, as components of antibacterial  
 CC vaccines, as targets for antibacterial drugs, to detect the presence of  
 CC A. baumannii and other Acinetobacter species in a sample, in screening  
 CC compounds for the ability to interfere with the A. baumannii life cycle  
 CC or to inhibit A. baumannii infection, and as biocontrol agents for  
 CC plants. The present sequence represents the amino acid sequence of an A.  
 CC baumannii protein.

XX Sequence 299 AA;

Query Match 53.0%; Score 106; DB 6; Length 299;  
 Best Local Similarity 52.9%; Pred. No. 9.6e-07;  
 Matches 18; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 FLGLGLMGSGIVSNLLKMGHTVTWNRATKCD 34  
 DB 14 GFVGIGMGPMWAMNLLKAGHQIKVWNRSSKAE 47

RESULT 20

ABU17066  
 ID ABU17066 standard; protein; 290 AA.

XX AC ABU17066;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #2593.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

KW Acinetobacter baumannii.

PN WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITFA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.

DR N-PSDB; ACA20936.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 44990; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 290 AA;

Query Match 52.5%; Score 105; DB 6; Length 290;  
Best Local Similarity 59.4%; Pred. No. 1.3e-06;  
Matches 19; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FLGLGLMGSGIVSNLLKMGHTVTVMRTAEK 32  
||:||||:||||:||||:||||:|  
Db 5 GFVGTGIMGMPMAMNLLKAGHQVKNRITSSK 36

RESULT 21  
ADA36852  
ID ADA36852 standard; protein; 326 AA.

XX AC ADA36852;

XX DT 20-NOV-2003 (first entry)

XX DE Acinetobacter baumannii protein #4013.

XX DE Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;  
XX KW plant biocontrol agent.

XX OS Acinetobacter baumannii.

XX OS US6562958-B1.

XX PN 13-MAY-2003.

XX PF 04-JUN-1999; 99US-00328352.

XX PR 09-JUN-1998; 98US-0088701P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Breton G, Bush D;

XX DR WPI; 2003-576092/54.

XX DR N-PSDB; ADA32726.

XX PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
XX PT for diagnosing a bacterial disease, as components of antibacterial  
XX PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
XX PT plants.

XX PS Example; SEQ ID NO 8139; 328pp; English.

XX CC The invention relates to isolated Acinetobacter baumannii nucleic acids.  
XX CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
XX CC for diagnosing a bacterial disease, as components of antibacterial  
XX CC vaccines, as targets for antibacterial drugs, to detect the presence of  
XX CC A. baumannii and other Acinetobacter species in a sample, in screening  
XX CC compounds for the ability to interfere with the A. baumannii life cycle  
XX CC or to inhibit A. baumannii infection, and as biocontrol agents for  
XX CC plants. The present sequence represents the amino acid sequence of an A.  
XX CC baumannii protein.

XX SQ Sequence 326 AA;

Query Match 51.0%; Score 102; DB 6; Length 326;  
Best Local Similarity 52.8%; Pred. No. 4.1e-06;  
Matches 19; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 FLGLGLMGSGIVSNLLKMGHTVTVMRTAEKDLFI 37  
||:||||:||||:||||:||||:|  
Db 49 FLGLGLMGSRMASRLIQAGFQVAVNRTTSACEELI 84

RESULT 22

AAG10425

ID AAG10425 standard; protein; 285 AA.

XX AC AAG10425;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 8741.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 23-MAR-1999; 99US-0123548P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 16-APR-1999; 99US-0128714P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 18-MAY-1999; 99US-0134370P.

XX PR 19-MAY-1999; 99US-0134941P.

XX PR 20-MAY-1999; 99US-0135124P.

XX PR 21-MAY-1999; 99US-0135353P.

XX PR 24-MAY-1999; 99US-0135629P.

XX PR 25-MAY-1999; 99US-0136021P.

XX PR 27-MAY-1999; 99US-0136392P.

XX PR 28-MAY-1999; 99US-0136782P.

XX PR 01-JUN-1999; 99US-0137222P.

XX PR 03-JUN-1999; 99US-0137528P.

XX PR 04-JUN-1999; 99US-0137502P.

XX PR 07-JUN-1999; 99US-0137724P.

XX PR 08-JUN-1999; 99US-0138094P.

XX PR 10-JUN-1999; 99US-0138540P.

XX PR 10-JUN-1999; 99US-0138847P.

XX PR 14-JUN-1999; 99US-0139119P.

XX PR 16-JUN-1999; 99US-0139452P.

XX PR 16-JUN-1999; 99US-0139453P.

XX PR 17-JUN-1999; 99US-0139492P.

XX PR 18-JUN-1999; 99US-0139454P.

XX PR 18-JUN-1999; 99US-0139455P.

XX PR 18-JUN-1999; 99US-0139456P.

XX PR 18-JUN-1999; 99US-0139457P.





19-JUN-2003 (first entry)  
Protein encoded by Prokaryotic essential gene #15494.  
Antisense; prokaryotic essential gene; cell proliferation; drug design.  
Enterococcus faecium.  
MO200277183-A2.  
03-OCT-2002.  
21-MAR-2002; 2002WO-US009107.  
21-MAR-2001; 2001US-00815242.  
06-SEP-2001; 2001US-00948993.  
25-OCT-2001; 2001US-0342923P.  
08-FEB-2002; 2002US-00072851.  
06-MAR-2002; 2002US-0362699P.  
(ELIT-) ELITRA PHARM INC.  
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
WPI; 2003-029926/02.  
N-PSDB; ACA33837.  
New antisense nucleic acids, useful for identifying proteins or screening  
for homologous nucleic acids required for cellular proliferation to  
isolate candidate molecules for rational drug discovery programs.  
Claim 25; SEQ ID NO 57891; 1766pp; English.  
The invention relates to an isolated nucleic acid comprising any one of  
the 6213 antisense sequences given in the specification where expression  
of the nucleic acid inhibits proliferation of a cell. Also included are:  
(1) a vector comprising a promoter operably linked to the nucleic acid  
encoding a polypeptide whose expression is inhibited by the antisense  
nucleic acid; (2) a host cell containing the vector; (3) an isolated  
polypeptide or its fragment whose expression is inhibited by the  
antisense nucleic acid; (4) an antibody capable of specifically binding  
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
proliferation or the activity of a gene in an operon required for  
proliferation; (7) identifying a compound that influences the activity of  
the gene product or that has an activity against a biological pathway  
required for proliferation, or that inhibits cellular proliferation; (8)  
identifying a gene required for cellular proliferation or the biological  
pathway in which a proliferation-required gene or its gene product lies  
or a gene on which the test compound that inhibits proliferation of an  
organism acts; (9) manufacturing an antibiotic; (10) profiling a  
compound's activity; (11) a culture comprising strains in which the gene  
product is overexpressed or underexpressed; (12) determining the extent  
to which each of the strains is present in a culture or collection of  
strains; or (13) identifying the target of a compound that inhibits the  
proliferation of an organism. The antisense nucleic acids are useful for  
identifying proteins or screening for homologous nucleic acids required  
for cellular proliferation to isolate candidate molecules for rational  
drug discovery programs, or for screening homologous nucleic acids  
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
the target prokaryotic essential genes. Note: The sequence data for this  
patent did not form part of the printed specification, but was obtained  
in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

Db 4 GFITGVMGSAVARHLLLEAGHEVAVYNRTAKAD 37  
RESULT 24  
ADC95482  
ID ADC95482 standard; protein; 299 AA.  
XX  
AC ADC95482;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE E. faecium protein sequence SEQ ID 5109.  
XX  
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;  
abdominal-pelvic infection.  
XX  
OS Enterococcus faecium.  
XX  
PN US6583275-B1.  
XX  
PD 24-JUN-2003.  
XX  
PF 30-JUN-1998; 98US-00107532.  
XX  
PR 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2003-799836/75.  
DR N-PSDB; ADC91828.  
XX  
PT New isolated nucleic acid derived from Enterococcus faecium encoding an  
Enterococcus faecium polypeptide useful for detection, prevention and  
treatment of a pathological condition resulting from a bacterial  
infection.  
XX  
PS Example 1; SEQ ID NO 5109; 243pp; English.  
XX  
CC The invention relates to an isolated nucleic acid derived from  
Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
one of 10 fully defined sequences given in the (for comprising 40  
sequential nucleotides chosen from any of the nucleic acids, its  
complement or sequences hybridising to it). Also included are a  
recombinant vector comprising the nucleic acid operably linked to  
transcription regulatory element, a cell comprising the vector and a  
single-stranded probe comprising the nucleic acid. The nucleic acids are  
chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids is useful for diagnosing pathological conditions  
resulting from E. faecium bacterial infection (e.g. urinary tract  
infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
infection) and for screening drugs such as agonists and antagonists. The  
nucleic acid is useful for recombinant production of Candida albicans -  
derived peptides or antisense polypeptides. Pharmaceutical compositions  
and vaccines containing the nucleic acid are useful for preventing or  
treating Enterococcus faecium infections. The present sequence represents  
one if the disclosed E. faecium proteins.  
XX  
SQ Sequence 299 AA;  
Query Match 50.0%; Score 100; DB 7; Length 299;  
Best Local Similarity 52.9%; Pred. No. 7.1e-06;  
Matches 18; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRTAKCD 34  
Db 8 GFITGVMGSAVARHLLLEAGHEVAVYNRTAKAD 41  
RESULT 25

DT 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #15494.  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Enterococcus faecium.  
XX MO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
XX 25-OCT-2001; 2001US-0342923P.  
XX 08-FEB-2002; 2002US-00072851.  
XX 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA33837.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 57891; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the  
XX proliferation of an organism. The antisense nucleic acids are useful for  
XX identifying proteins or screening for homologous nucleic acids required  
XX for cellular proliferation to isolate candidate molecules for rational  
XX drug discovery programs, or for screening homologous nucleic acids  
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
XX the target prokaryotic essential genes. Note: The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 295 AA;  
Query Match 50.0%; Score 100; DB 6; Length 295;  
Best Local Similarity 52.9%; Pred. No. 7e-06;  
Matches 18; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
QY 1 GFLGLMGSGIVSNLLKMGHTVTWNRTAKCD 34

AAW27613

ID AAW27613 standard; protein; 492 AA.

XX AC AAW27613;

XX DT 22-DEC-1997 (first entry)

XX DE Brevibacterium flavum 6-phosphogluconate dehydrogenase.

XX KW Brevibacterium flavum; 6-phosphogluconate dehydrogenase;

XX RW recombinant production; coryneform; bacterium; bacteria.

XX OS Brevibacterium flavum.

XX PN JP09224662-A.

XX PD 02-SEP-1997.

XX PF 23-FEB-1996; 96JP-00036346.

XX PR 23-FEB-1996; 96JP-00036346.

XX FA (MITU) MITSUBISHI CHEM CORP.

XX DR WPI; 1997-484097/45.

XX DR N-PSDB; AAT86035.

PT 6-phosphogluconate dehydrogenase - can be recombinantly produced by transforming coryneform bacteria with DNA molecule encoding it.

PS Claim 1; Page 5-7; 8pp; Japanese.

CC The present sequence is the Brevibacterium flavum JM-233 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be recombinantly produced by transforming coryneform bacteria with the DNA molecule encoding it

XX SQ Sequence 492 AA;

Query Match

Best Local Similarity 46.5%; Score 93; DB 2; Length 492;

Matches 17; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 GFLGLGLMGSGIVSNLLKMGHTVTVMNRATPKCDLFI 37

Db 19 GVVGGLAVMGSLNARNFARNGHTVAVYKRSYDXTDKLI 55

RESULT 26

AAG06417

ID AAG06417 standard; protein; 158 AA.

XX AC AAG06417;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 3182.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX RW hybridisation assay; genetic mapping; gene expression control; promoter;

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137528P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 02-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

|    |              |                  |
|----|--------------|------------------|
| PR | 16-JUL-1999; | 99JUS-01444085P; |
| PR | 16-JUL-1999; | 99JUS-01444086P; |
| PR | 19-JUL-1999; | 99JUS-01444325P; |
| PR | 19-JUL-1999; | 99JUS-01444331P; |
| PR | 19-JUL-1999; | 99JUS-01444332P; |
| PR | 19-JUL-1999; | 99JUS-01444333P; |
| PR | 19-JUL-1999; | 99JUS-01444334P; |
| PR | 19-JUL-1999; | 99JUS-01444352P; |
| PR | 20-JUL-1999; | 99JUS-01444632P; |
| PR | 20-JUL-1999; | 99JUS-01444884P; |
| PR | 21-JUL-1999; | 99JUS-0144816P;  |
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DT 17-OCT-2000 (first entry)
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KW termination sequence.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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XX PF 25-FEB-2000; 2000EP-00301439.
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